



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 124854

TO: Manjunath N Rao
Location: REM-3B81/3C70
Art Unit: 1652
Friday, June 18, 2004

Case Serial Number: 10/038723

From: Mary Jane Ruhl
Location: Biotech-Chem Library
Remsen 1-A-62
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

Search Notes

Examiner Rao,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl
Technical Information Specialist
STIC
Remsen 1-A-62
Ext. 22524

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From: Chan, Christina
Sent: Wednesday, June 16, 2004 5:28 PM
To: Rao, Manjunath N.; STIC-Biotech/CheMlib
Subject: RE: RUSH sequence search request for 10/038,723

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 & 1642
(571)-272-0841
Remsen, 3E89

-----Original Message-----

From: Rao, Manjunath N.
Sent: Wednesday, June 16, 2004 10:51 AM
To: Chan, Christina
Subject: RUSH sequence search request for 10/038,723

Hello Christina,

Please authorize the request below as RUSH. The reason being , this is an amended case and due this bi-week.

Thanks
-Manjunath

From: Manjunath N. Rao
Art Unit 1652, Room 3B81
Mail Box in Room 3C70
Phone: 272-0939

Date: 6-16-04

Please search the following as soon as possible for application with serial number
10/038,723

1. SEQ ID NO: 2 and amino acids 1-295 against all commercial amino acid databases,
issued patents/published applications database and pending application

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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database. Please provide a print of all results.

If you have any questions please call me at the above phone number.

Thanks

Manjunath N. Rao
Art Unit 1652, Room 3B81,
Mail Box in Room 3C70,
Remsen Building, USPTO
400, Dulany St.
Alexandria, VA.
Phone: 571-272-0939

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 17, 2004, 17:43:18 ; Search time 20 Seconds

Perfect score: 2771 (without alignments)

Sequence: 1 MSFRSLALSGLVCTGLANV.....SKTTATASKTSTTRSGMSL 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Listing first 45 SummariesDatabase : PIR_78,*
1: pir1,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2771	100.0	534	A29776	glucan 1,4-alpha-glucosidase (EC 3.2.1.3) G2 precursor - Aspergillus awamori
2	2742	99.0	640	1 ALASGR	N;Alternate names: glucomylase G2
3	2742	99.0	640	2 A29166	C;Species: Aspergillus awamori
4	2620	94.6	639	2 J00607	C;Date: 20-Jun-1989 #sequence_revision 20-Jun-1989 #text_change 12-Jun-2003
5	2588	93.4	639	2 JT0479	R;Numberg, J.H.; Meade, J.H.; Cole, G.; Lawyer, F.C.; McCabe, P.; Schweickart, V.; Tal, A;Title: Molecular cloning and characterization of the glucoamylase gene of Aspergillus
6	1935	69.8	612	2 JQ1346	A;Reference number: A93066; MUID:85085934; PMID:6440004
7	1577	56.9	626	2 S36364	A;Reference number: A93066
8	1577	56.9	626	2 T49625	A;Accession: A93066
9	1497	54.0	493	2 JC6538	A;Molecule type: DNA
10	1321	47.7	616	2 S33908	A;Residues: 1-534 <NUN>
11	781.5	20.2	450	2 T39433	A;Cross-references: GB:K02465; PIDN:9454405; PIDN:AB59297.1; PID:9166505
12	724	26.1	604	1 JP0001	R;Numberg, J.H.; Meade, J.H.; Cole, G.; Lawyer, F.C.; McCabe, P.; Schweickart, V.; Tal, A;Reference number: A94514
13	676.5	24.4	519	1 A54549	A;Contents: annotation; revisions to the DNA sequence and coding regions for G2 form
14	597	21.5	549	1 S48474	C;Comment: The DNA sequence was obtained from Genbank, release 55.0.
15	522	18.8	778	1 AUBYG	C;Superfamily: glucan 1,4-alpha-glucosidase homologs
16	521	18.8	767	1 JT0474	C;Keywords: alternative splicing; extracellular protein; glycoprotein; glycosidase; hydrolytic enzymes; homologs; homology <GAG>
17	221.5	8.0	615	2 A64501	F;23-447/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
18	181	6.5	1588	2 A86306	Query Match 100.0%; Score 2771; DB 2; Length 534;
19	6.5	1588	2 H9118B	Best Local Similarity 100.0%; Pred. No. 5.9e-179;	
20	172	6.2	622	2 G90250	Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
21	170.5	6.2	1275	2 T33369	Db
22	166.5	6.0	107	2 B60754	QY 1 MSFRSLALSGLVCTGLANVSKRATDSLNEATVARTAILNNIGADCAWVGSGRDSGI 60
23	161	5.8	1063	2 D86731	Db 1 MSFRSLALSGLVCTGLANVSKRATDSLNEATVARTAILNNIGADCAWVGSGRDSGI 60
24	5.8	888	2 T46726	Db 61 VVASSTDNTDPDYFTWTRDGLVLTIVLDFRNQDTSLAINTYQAIVQGINSNPG 120	
25	5.7	1210	2 A25547	Db 121 DLSSGAGLGPKFNNDTETAVGSMQRQRDGPALRATAMIGFGQWLLDNQTSSTATIDW 180	
26	159	5.7	2271	2 F90073	Db 121 DLSSGAGLGPKFNNDTETAVGSMQRQRDGPALRATAMIGFGQWLLDNQTSSTATIDW 180
27	158	5.7	1283	2 T39174	Db 181 PLVRNDLSIYQAQWNQQTGTDLWEEBNGSSFTIAVQHRALVEGSAFATAVGSSCSWCDSQ 240
28	5.7	1258	2 JQ0174	Db 241 APEILCYLGSFWTESFLANDFDSRSKGKANTLGSIHDFPDEACDSTFQESPRAIA 300	
29	5.6	2232	2 T34434	Db 241 APEILCYLGSFWTESFLANDFDSRSKGKANTLGSIHDFPDEACDSTFQESPRAIA 300	

ice nucleation pro
ice nucleation pro
hypothetical serin
ice nucleation act
MS2B protein - Yea
mann endo-1,4-beta
probable membrane
hypothetical prote
probable membrane
glucan 1,4 alpha g
hypothetical prote
aglutinin-like ad
endo-1,4-beta-xyla
hypothetical prote
ice nucleation pro

RESULT 2

ALASGR
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus niger
 N:Alternative names: 1,4-alpha-D-glucan glucohydrolase; glucoamylase
 C:Species: Aspergillus niger
 C:Accession: 28-Dec-1987 #sequence revision 28-Dec-1987 #text_change 02-Jun-2003
 R:Boel, E.; Hansen, M.T.; Hjort, I.; Hoegh, J.; Friis, N.P.
 EMBO J. 3, 1581-1585, 1984
 A:Title: Two different types of intervening sequences in the glucoamylase gene from Aspergillus niger
 A:Reference number: A90986; MUID:8426458; PMID:6204865
 A:Accession: A90986
 A:Molecule type: DNA
 A:Residues: 1-640 <S>R>
 A:Cross-references: GB:X00712; GB:K02466; NID:92342; PIDN:CAA25303_1; PID:g2343
 R:Svensson, B.; Larsen, K.; Gunnarsson, A.
 Eur. J. Biochem. 154, 497-502, 1986
 A:Title: Characterization of a glucoamylase G2 from Aspergillus niger.
 A:Reference number: A91161; MUID:86136085; PMID:3081341
 A:Contents: comparison of forms G1 and G2
 A:Accession: A91161
 A:Molecule type: protein
 A:Residues: 25-640 <S>R>
 C:Comment: The large molecular form G1 is shown.
 C:Comment: Smaller molecular forms of the enzyme, G2, arise by proteolytic cleavage(s) competitive towards soluble poly- and oligosaccharides.
 C:Genetics:
 A:Introns: 72/1; 167/3; 200/1; 412/3
 C:Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase; glycoprotein; glycosidase; hydrolase; alpha-1-24-domain; signal sequence #status predicted <SIG>
 F:23-447/Domain: glucan 1,4-alpha-glucosidase homology <SGH>
 F:25-640/Product: glucan 1,4-alpha-glucosidase G1 #status experimental <GG1>
 F:25-538/Product: glucan 1,4-alpha-glucosidase G2, short form #status experimental <GG3>
 F:25-536/Product: glucan 1,4-alpha-glucosidase G2, long form #status experimental <GG2>
 F:419-419/Binding site: carbohydrate (ASN) (covalent) #status experimental <GG3>
 F:465,467,468,477,483,484,492,508,510,513,515,522,525,527,529,530,532/Binding site: carbohydrate (ASN) (covalent) #status experimental <GG3>
 F:476,486,488,496,499,500,501,502,504,506,512,514,517,518,520,524,526,528,531,534,535/Bi
 Query Match 99.0%; Score 2142; DB 1; Length 640;
 Best Local Similarity 99.6%; Pred. No. 6.8e-177;
 Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSFRSLLALSGLVGTGLANVISKRTATLPSWLSNEAVTARTAIIANIGADGAWVSGADSGI 60
 1 MSFRSLLALSGLVGTGLANVISKRTATLPSWLSNEAVTARTAIIANIGADGAWVSGADSGI 60
 QY 61 WVASPSTNDPYFTWTRDGLVLTKLVLFRNGDTSLISTIENYISQAIVQGINSNSPG 120
 61 WVASPSTNDPYFTWTRDGLVLTKLVLFRNGDTSLISTIENYISQAIVQGINSNSPG 120
 121 DLSSGAGLGEPKFENDTAYTGSGRPQDGPAKARATAMIGFGWQMLDGYNSTATDIW 180
 121 DLSSGAGLGEPKFENDTAYTGSGRPQDGPAKARATAMIGFGWQMLDGYNSTATDIW 180
 181 PLYVRNLDSVVAQYNNQQTGIDLWEERNNGSFTAVQHRLAVERGSGAFATAVGSSCSCWCSQ 240
 181 PLVNRNLDSVVAQYNNQQTGIDLWEERNNGSFTAVQHRLAVERGSGAFATAVGSSCSCWCSQ 240

RESULT 4

JQ0607
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - *Aspergillus* sp.
N;Alternative names: glucanomylase
C;Species: Aspergillus sp.

C-Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 02-Jun-2003
C;Accession: JQ0607
R;Shibuya, I.; Gomi, K.; Timura, Y.; Takahashi, K.; Tamura, G.; Hara, S.
A;Title: Molecular cloning of the glucamylase gene of *Aspergillus shirouسامي* and its expression in *Saccharomyces cerevisiae*
A;Reference number: JQ0607; Muiin:91102400; PMID:1136803
A;Accession: JQ0607
A;Molecule type: DNA
A;Residue: 1-639 <SHI>
A;Experimental source: strain RIB 2504
C;Comment: This enzyme catalyzes the release of glucose from the non-reducing ends of starch.
C;Genetics:
A;Introns: 72/1; 16/6/3; 199/1; 41/3
C;Superfamily: Glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-glucosidase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-4/Domain: signal sequence #status predicted <SIG>
F;23-469/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
F;25-639/#Product: glucoamylase #status predicted <MAT>

Query Match	94.6%	Score 2620.5;	DB 2;	Length 639;
Best Local Similarity	94.3%	Pred. No. 1e-168;		
Matches 500;	Conservative	16;	Mismatches 13;	Indels 1;
				Gaps 1;
Qy	1 MSFRSLLALSLGLVGLTGLANVISKRTATLDSWLSNTAVARTAILNNIGADGAWSGADSGI	60		
Db	1 MSFRSLLALSLGLVGLTGLANVISKRTATLDSWLSNTAVARTAILNNIGADGAWSGADSGI	60		
Qy	61 VVASPSTONPDYFTWTDGLVLTLDLPRFGDTSLISTENIISADAIVOGINSRPG	120		
Db	61 VVASPSTONPDYFTWTDGLVLTLDLPRFGDTSLISTENIISADAIVOGINSRPG	120		
Qy	121 DLSSGAGLGEPKENVEDAYTGSGKRPQDGPAKATAMIGFGQWMLDQYTSRATDIW	180		
Db	121 DLSSGAGLGEPKENVEDAYTGSGKRPQDGPAKATAMIGFGQWMLDQYTSRATDIW	180		
Qy	181 PLVRNDLISYVAQWNWQTGYDLWEEWNGSFFTAIVQHRALEVEGAAFAATAVGSSSSWCDSQ	240		
Db	180 PLVRNDLISYVAQWNWQTGYDLWEEWNGSFFTAIVQHRALEVEGAAFAATAVGSSSSWCDSQ	239		
Qy	241 APRILCYIQSFWFGSFTIANFDSSRSRGKDANTLIGSIHTDPPEACADDSTFOPCSRALA	300		
Db	240 APOILCTIQSFWFGSFTIANFDSSRSRGKDANTLIGSIHTDPPEACADDSTFOPCSRALA	299		
Qy	301 NHKEVWPSRSYVTLNDGLSDSEAWAVRYPEDTYNGNPWELCTLAEEQYDLYQMD	360		
Db	300 NHKEVWPSRSYVTLNDGLSDSEAWAVRYPEDTYNGNPWELCTLAEEQYDLYQMD	359		
Qy	361 KQCSLEVTDLDPFKALYSDAATGTYSSSSSTISIVDAVKPFDGFVISIVETHASNG	420		
Db	360 KQCSLEVTDLDPFKALYSDAATGTYSSSSSTISIVDAVKPFDGFVISIVETHASNG	419		
Qy	421 SMSEQYDKSDGEQLSARDITWSYALLTANNRRNNSVVPASWGETSASSVPGTCATSAIG	480		
Db	420 SMSEQYDKSDGEQLSARDITWSYALLTANNRRNNSVVPASWGETSASSVPGTCATSAIG	479		

QY
Db
RESULT 5
JT0479 481 TWSVTWTSWPSTVATGGTTATPTGSGSVTSTSITTA
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus awamori
N Alternative names: glucosidase I
C Species: *Aspergillus awamori*
C Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 02-Jun-2003
C Accession: JT0479
R Hayashida, S.; Kuroda, K.; Ohta, K.; Kuwara, S.; Fukuda, K.; Sakai, Y.
Agric. Biol. Chem. 53, 923-929, 1989
A Title: Molecular cloning of the glucosidase I gene of *Aspergillus awamori* var. kawachi
A Reference number: JT0479
A Accession: JT0479
A Molecule type: DNA
A Residues: 1-639 <HAY>
A Experimental source: var. kawachi
C Genetic:
A Gene: GAI
A Introns: 72/1; 166/3; 199/1; 411/3
C Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha
C Keywords: glycosidase; hydrolase; polysaccharide degradation
P; 1-24/Domain: signal sequence #status predicted <SIG>
F; 23-44/Domain: glucan 1,4-alpha-glucosidase homology <GGG>
F; 25-639/Product: glucan 1,4-alpha-glucosidase #status predicted <MAT>
F; 494-538/Region: raw-starch-affinity region

glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - *Aspergillus oryzae*
 N;Alternate names: glucoamylase
 C;Species: *Aspergillus oryzae*
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 02-Jun-2003
 C;Accession: JQ0146
 R;Hata, Y.; Tsuchiya, K.; Kitamoto, K.; Gomi, K.; Kumagai, C.; Tamura, G.; Hara, S.
 Gene 108, 145-150, 1991
 A;Title: Nucleotide sequence and expression of the glucoamylase-encoding gene (glaA) from *R. Japonicus*
 A;Reference number: JQ0146; MUID:9210497; PMID:1761224
 A;Accession: JQ0146
 A;Molecule type: DNA
 A;Residues: 1-612 <HAT>
 A;Cross-references: GB:D1098; DDBJ:001108; NID:91160312; PIDN:BA01540.1; PID:91160313
 A;Note: The authors translated the codon TTT for residue 213 as Tyr
 C;Comment: This enzyme hydrolyzes starch to glucose.
 C;Genetics:
 A;Gene: glaA
 A;Introns: 75/1; 169/3; 202/1; 414/3
 C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-F;26-449/Domain: glucan 1,4-alpha-glucosidase homology
 Query Match 69.8%; Score 1335; DB 2; Length 612;
 Best Local Similarity 70.3%; Pred. No. 1-4e-122;
 Matches 367; Conservative 59; Mismatches 90; Indels 6; Gaps 4;
 QY 1 MSRSLLALSGLVCTGLA--NVISKRATIDSWSNEATVARTATLNNIGADGAWVGADS 58
 Db 2 VSFSCLRALGSSVLAVQPVLRQATGLDTWLSTEAMFSRQATINNIGADGOSAQGASP 61
 QY 59 GIWVAPSPSTDNPDXFYTWRDGSVLUKTLVDFRNGDPSLSTIENYISAQAVQGISN 118
 Db 62 GWVIASPKSDPDYFTWTRDGLVMKTLVDFRGGDADLPIEEFISQARIQNSP 121
 QY 119 SGDLSSGAGLGEPEKVNDETAATGSGWGRQRDGPAALRATAMIGFGQWILDNGYSTATDI 178
 Db 122 SGALSS-G-LGERPEKVNDETAATGAWGRFQDSPALRATAMISFGEWLNHSIARDL 180
 QY 179 VWPVLVRNDISYVAQIYWNQTDGYDIFMEEVNGSSFFTIAVORHALVEGSAFATAVQSSCSWCD 238
 Db 181 VWPVFRNDISYVAQIYWNQSGFDPDWEEVQOTTSFFAVASIRALVEGSSPAKTVQSCPCD 240
 QY 239 SQAPEILCYLQLQSFWTGSGPFLANFDSSRSCKDANTLGSHTFPEAACDSTFOPCSRA 298
 Db 241 SQAPQVRCYLQLQSFWTGSGIYQANFEGGRGRSKDINVLGSLHTFPEQATFOPCSARA 300
 QY 299 LAMHEKVUDSFRSYTTLNGLSDSEAIVAVGRYPTDITGNPWFCTLAAGEQLYDALQ 358
 Db 301 LAMHKVUDTSFRSYTTLNGLSDSEAIVAVGRYPTDITGNPWFCTLAAGEQLYDALQ 360
 QY 359 WDKGQSLETDVSDLDPFKALYSDAATGTYSSSSSTYSSITDVAVKTFADGFVSVETHAS 418
 Db 361 WDKGQSLATDVSUPLPFKALYSSAAATGTYASSTIVYKOLIVSAKAVAGYQVQVTVAS 420
 QY 419 NGMSBQYKSGDQLSANDLTWSYALLTANRNNSVPPASNGCETSSAASSVPGCAATSA 478
 Db 421 TGSMAEQYTKIDGSQTSARDLTWSYALLTANRNNAVVPAGMGTAAATSIAPSACSTSA 480
 QY 479 IGYTSSVWVNTWSIVATGCT--TTAATPGSGSVTSKTT 518
 Db 481 SGTYSSVVITSWPRTSGYGPAPSPCQVPT-TVSUTFAVKA 521
 RESULT 7
 S36364 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - *Neurospora crassa*
 C;Alternate names: glucoamylase; glycoamylase
 C;Species: *Neurospora crassa*
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2003
 C;Accession: S36364; S13710; S13711; S25539
 R;Stone, P.J.; Makoff, A.J.; Parish, J.H.; Radford, A.
 Curr. Genet. 24, 205-211, 1993
 A;Title: Cloning and sequence analysis of the glucoamylase gene of *Neurospora crassa*.

A;Reference number: S16364; MUID:94037144; PMID:8221928
 A;Accession: S16364
 A;Molecule type: DNA
 A;Residues: 1-625 <STOP>
 A;Cross-references: EMBL:X67291
 R;Koh-Jaur, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Airley, K.; Johansen, F.E.
 Enzyme Microb. Technol. 11, 692-695, 1989
 A;Title: Exported proteins of *Neurospora crassa*: 1-glucoamylase.
 A;Reference number: S13710
 A;Accession: S1710
 A;Molecule type: protein
 A;Residues: 36-60, X', 62, X', 64-65 <KOH>
 R;Koh-Jaur, S.I.; Parish, J.H.; Bleasby, A.J.; Pappin, D.J.C.; Airley, K.; Johansen, F.E.
 Submitted to the Protein Sequence Database, January 1990
 A;Description: Exported proteins of *Neurospora crassa* 1: - glucoamylase.
 A;Reference number: S13711
 A;Accession: S13711
 A;Molecule type: protein
 A;Residues: 36-60, X', 62, X', 64-65 <KOW>
 C;Genetics:
 A;Gene: gla-1
 A;Introns: 82/2
 C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha-F;20-35/Domain: signal sequence #status predicted <SIG>
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
 F;33-438/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F;36-626/Product: glucan 1,4-alpha-glucosidase #status experimental <MAT>
 Query Match 56.9%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 1-9e-98;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;
 QY 2 SFRSLLALSGLVCTGLANVISKEATLWSLNEATVARTATLNNIGADGAWVGADS 61
 Db 13 AFQVGLGDPDPLKEKRSIDIKR-SVSIYQNETPQAKNLICGAGCRASGAAGCW 71
 Query Match 57.6%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 1-9e-98;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;
 QY 62 VASPSTDNPDXFYTWRDGSVLUKTLVDFRNG-DTSLSLTIENYISAQAVQGISN 120
 Db 72 VASPSKSSPDYWTWTRDALKLIVDEFTNDYNTTQINTQAYAAQAKLOGVSNB 131
 QY 121 DLSSGAGLGEPEKVNDETAATGSGWGRQRDGPAALRATAMIGFGQWILDNGYSTATDIW 180
 Db 132 SLNGAGLGEPEKVNDETAATGAWGRFQDSPALRATAMISFGEWLNHSIARDL 191
 QY 181 PLVTRNDISYVAQIYWNQTDGYDIFMEEVNGSSFFTIAVORHALVEGSAFATAVQGSCSWCWSQ 240
 QY 192 PIYKNDLIAATQWNNTDFLWREVNSESSFTIAASHRHLVEGSAFAKSGVGSCSACDAI 251
 Db 241 APEILCYQSFWFGS-FTIANFDSSRSCKDANTLGSHTFPEAACDSTFOPCSPRAL 299
 Db 252 APOICFOQSFWSNSGTYISNFVNRSKCDINSVLTSHNFPAAGCDVNTFOPCSDR 311
 QY 300 ANHEKVUDTSFRSYTTLNGLSDSEAIVAVGRYPTDITGNPWFCTLAAGEQLYDALQW 359
 Db 312 ANHKVUDSMR-FWGVNQGRTACKAAGVYARDVYINGPNPWLTAAEQLYDALYW 370
 QY 360 DKQGSLETDVSDLDPFKALYSDAATGTYSSSSSTYSSITDVAVKTFADGFVSVETHAS 419
 Db 371 KKQGSITITSLAFLPKLQVPSVSTGIGYSSSSSTYTAIINATYYAQGVFDIVAQYFSD 430
 QY 420 GSMSQYKSGDQLSADLTMWSYALLTANRNNSVPPASNGCETSSAASSVPGCAATSA 479
 Db 431 GSLAEQFDKDSGAPLSAATHLTWSYASELUSAARRAGTVPPSWGASAANSLPGSCSASTWA 490
 QY 480 GTSSSVTTSWPSIVATGCTT-AIPGSGS----VTSKTTATASKT 524
 Db 491 GSYATATTSPPNLTPTASTVPPPTQGCAADHEVLFVTNEKVTTSQGQT 541
 RESULT 8
 T9625 glucan 1,4-alpha-glucosidase [Imported] - *Neurospora crassa*

N;Alternate names: protein B5022.70
 C;Species: Neurospora crassa
 C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2003
 C;Accession: M49625
 R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 R;Reference number: 225022
 A;Accession: T99625
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-626 <SCH>
 A;Cross-references: EMBL:AL355932; GSPDB:GN00116; NCSP:B5022.70
 A;Experimental source: BAC clone B5022; strain OR74A
 C;Genetics:
 A;Gene: NESP:B5022.70
 A;Map position: 6
 A;Introns: 82/1
 C;Superfamily: glucan 1,4-alpha-glucosidase with starch-binding domain; glucan 1,4-alpha
 Query Match Best Local Similarity 56.9%; Score 1577; DB 2; Length 626;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;
 QY 2 SPRSLUALSGVCTGLANVSKRATLSWISNEATVARTAILNNGADGAWVGAGDSIV 61
 13 AFQAVLGLPDPPLHEKRHSIDTR-SVDSVYCIPTPIAQKNLICNIGASGRASGRASGVV 71
 QY 62 WASPSTONPDYFTWTRDGSVLUKTLVLDFRNG-DTSLLSTENIYISAQAVQGNSNPNG 120
 72 VASPKSSPPDWYTWDRDAALVTKLJDEFNDYNTQLONTQAYAAQALQVSNPSC 131
 QY 121 DLSGGAGLGEPKPNVDEATVATGSGRPQRDGPALARATAMICPGQWMLDNGYTTANDIV 180
 132 SLSNAGAGLGERKFMDVLQQFQAWGRPKRDGPPLRALIGSYKWLVSNGYADAKSIW 191
 QY 181 PLVRNLISYVQWNGTGYDIEWEENGSSRFITAVORHALVEAGSATAVOSSCSWCDQ 240
 192 PFLVKNDLAVTAYQWNNNTGFDLWEEVNNSSSFFTAASHRALVEGSAFAKSVSSCACAI 251
 Db 241 APRLCYLQSFHTGS_PILANFDSSRGKDANTLGSINTDPAAACDDSTFQPSRAL 299
 Db 252 APQLFQFQSNSVNSNQGKDNINSVTSIHNTDPAACDVNTFQPSDRAL 311
 QY 245 LCVLSFWTTSEFLANEDSS-RSGKDANTLGSINTDPAAACDDSTFOCSPRALNH 303
 Db 247 LCHLQDFWNGSAVLSNLPNTGRSGLDNTSLSIHTPDAACDDTTFOPCSRALSNHK 306
 QY 304 EWDSDRSITYLNGLSDSEAVAVGRYPEDTYNGNPWFCLTAAABOLYDALYKNDKQG 363
 Db 307 LVDSRSFWTTSEFLANEDSS-RSGKDANTLGSINTDPAAACDDSTFOCSPRALNH 366
 QY 364 SLEUTVSLOPDKALYSDAATGTYSSSSSTSYTIVDAVKTFADGFVISIVTHAASNMS 423
 Db 312 ANHKKVVDMSR_FWGVSNSGRTAGKAAVGRYADVIYNGNWLATAAKBOLYDavyW 370
 QY 360 DKQGSLSLVTDTSLDFEKFALYDAATGTYSSSSSTSYTIVDAVKTFRADGFVISIVEHAASN 419
 Db 371 KQKGSTTIVTSTSLLAFFKDLVPSVSTGTYSSTSSSYTATINAVTYADGFVIVDQTPSD 430
 QY 420 GSMSEQYDKSGOBQSLSARDLTTWSYALLTANRNNSVUPASWGETSASSVGTCAATSAI 479
 Db 431 GSLABOPDKDGAAPLATHLTWSYASFLSARRAGIVPPGWAANSLSLGSCSASTVA 490
 QY 480 GTYSSVTVTSNPSIVTGTTT-ATPTGSCS----VTSTSKTTATASKT 524
 Db 491 GSYATATATSPANLIPASTTVTPPIQTGCAADHEVLVTFENKEVTTSYQT 541
 RESULT 9
 JC6518 Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Aspergillus oryzae
 C;Species: Aspergillus oryzae
 C;Accession: M6338
 C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 12-Jun-2003
 C;Accession: P6503
 R;Hara, Y.; Isidra, H.; Ichikawa, E.; Kawato, A.; Sugimami, K.; Imaiayu, S.
 Gene 207, 127-134, 1998
 A;Title: Nucleotide sequence of an alternative glucoamylase-encoding gene (glab) express
 A;Reference number: JC6518; MUID:9017274; PMID:9511753
 A;Accession: P6503
 A;Molecule type: protein
 A;Residues: 43-53;71-82;136-145;180-187;327-336;393-404 <HAZ>
 RESULT 10
 S33908 Glucan 1,4-alpha-glucosidase (EC 3.2.1.3) P precursor - creosote fungus
 N;Alternate names: glucamylase
 C;Species: Amorphotheca resiniae, Hormoconis resiniae (creosote fungus)
 C;Accession: S33908
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-2003
 R;Vainio, A.E.I.; Torkkeli, H.T.; Tuuba, T.; Aho, S.A.; Fagerstroem, B.R.; Korhola, M.P.
 Curr. Genet. 24, 38-44, 1993
 A;Title: Cloning and expression of Hormoconis resiniae glucamylase P cDNA in Saccharomyces
 C;Reference number: S33908; MUID:9336503; PMID:8358830
 A;Accession: S33908
 A;Molecule type: mRNA
 A;Residues: 1-616 <VAL1>
 A;Cross-references: EMBL:X67708; NID:92785; PIDN:CAA47945.1; PID:92786
 A;Accession: S33677
 A;Molecule type: protein

A;Residues: 30-106-138-151;68-181;217-223;260-294;310-316;321-334;336-342;369-415;423-4
 R;Joutjoki, V.; Torkkeli, T.; R;Xiang, Z.; Aves, S.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
 submitted to the EMBL Data Library, August 1992
 A;Reference number: S31425
 A;Accession: S31425
 A;Molecule type: DNA
 A;Residues: 1-616 <JOU>
 A;Cross-references: EMBL:X68143; PIDN:CAM48243.1; PID:92788
 A;Residues: 30-53;72-89;145-154;217-223;260-294;423-426, 'X', 428-436 <FAg>
 A;Experimental source: strain ATCC 20495
 C;Genetics:
 A;Gene: gamp
 C;Superfamily: glucan 1,4-alpha-glucosidase, yeast type; glucan 1,4-alpha-glucosidase hon
 C;Keywords: glycoprotein; glycosidase; hydrolase; polysaccharide degradation
 F1-29/Domain: signal sequence #status predicted <SIG>
 F27-455/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F30-616/Product: glucan 1,4-alpha-glucosidase #status experimental <MAT>
 F499,427/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F200,514,528,587/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 47 %; Score 1321; DB 2; Length 616;
 Best local similarity 48 %; Pred No. 3.e-81; Mismatches 150; Indels 34; Gaps 6;
 Matches 257; Conservative 88; Mismatches 150; Indels 34; Gaps 6;
 QY 14 CTGLANVIS-----KRTALDSWSNEATVARTAILNNIGADGANVISGADSGIVVA 63
 8 CAGAISLLCSLATAAPTELKARDLSSFIASERATIAQALGANNICGPDSGAAPVGAGAFWVA 67
 Db 64 SPSTDNPDPYFTWTRDGLVLUKLVLDFRNGDTSLSLSTENYIQAQATVQGSNSPGD-L 122
 68 SPSPKANPDPYFTWSDSALTLMKIDFIGHTNLQTLIEQYHQAVIQTQVSPSGFL 127
 QY 123 SSGAGLGPERKPNVDETAYGSGWGRDGPRLATAMICPQWLDINGTSTANDIWPL 182
 128 PDGVQIGEPPKFMVDSGTRFGPFWGRQRDGPRALRAJALMYNSWLKNGFAEAKTKWPI 187
 Db 183 VRNDLSVYQWYQMNQTYDLYWEENGSSPFITAVPHRALVEGSAFATAVGSSCSWCDSDQAP 242
 188 IANDLSVYQGWNOQSGFDLWEETAYSSFFTIONQHARALVEGAQLAHDLGVTCTGCD-QAP 246
 QY 243 EILCULQSFWTFGSFLIANF--DSSRGKDANTLIGSIIHFPPEACDDSTFQPSRPLA 300
 247 EVILCFLOFSFNGKGYKIVINNWRGTLGDSNLSIGAISTFDIADYCDSPLOQPHQSLSA 306
 QY 301 NHKEVUDSFRSIYTTLGDSDESEAVALGVPEDTYGNPWFCLTLAAEQLDYLQYD 360
 Db 307 NFVKLTDTFRMLYTINAGIPEGQGVAVGRYKADEVYMGQWPLWLTAAEQLDYLQYD 366
 QY 361 KQGSLEVTDVSLDFEKKALYSDAATGTYSS--SSSTYSSITDAVKTIFADGFVSVETHAAS 418
 Db 367 ARHVLTVDTSLSLAFFRDIVPEFTVREYKSGNANSPFAQIMDAVAYADSYVATAEKYIPS 426
 QY 419 NGMSBQYDKDSGEQLSARDLTIWSYALLTANNRRNSVUPASWGETSASSVPGTCATSA 478
 427 NGSLSEQFNRTGTGTPSLAIDLTSWAFAFTTMSQRAGQPSWSMSRSRNALPPPTCSAST 486
 QY 479 IGTSSSVTVTWSWPSTIVATGGTTTAMPSTGSSGVSTSKTTASKTST 527
 Db 487 PGIV-----TPAAGAARNVSSCQSVITFINATT 517
 RESULT 12
 JP0001
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - Rhizopus oryzae
 Name: 1,4-alpha-D-glucan glucohydrolase; glucoamylase
 C;Species: Rhizopus oryzae
 C;Date: 28-Dec-1987 #sequence_revision 23-Aug-1996 #text_change 16-Jun-2000
 C;accession: JP0001
 R;Abeikiri, T.; Nakamura, N.; Tanaka, Y.; Kiuchi, N.; Shibano, Y.; Tanaka, T.; Amachi, T
 Agric. Biol. Chem. 50, 957-964, 1986
 Db 427 Rhioporus raw-starch-degrading glucoamylase: its cloning and expression in yeast
 A;Reference number: A90022
 A;Accession: JP0001
 A;Molecule type: DNA
 A;Residues: 1-604 <ASH>
 A;Cross-references: GB:D00049; PIDN:BAA00033.1; PID:9218035
 A;Experimental source: strain SW0034
 A;Note: there are two errors in the published sequence (personal communication): CCT (11c
 Y to the known amino acid sequence of 11 peptides from glucoamylase, including the amino
 R;Tanaka, Y.; Abeikiri, T.; Nakamura, N.; Kiuchi, N.; Shibano, Y.; Amachi, T.; Yoshizumi,
 Agric. Biol. Chem. 50, 965-969, 1986
 A;Title: Comparison of amino acid sequences of three glucoamylases and their structure-f
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jun-2003

RESULT 11
 T39433
 glucoamylase precursor - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 12-Jun-2003

A;Reference number: A90023
A;Contents: annotation; homology; predicted secondary structure
C;Comments: Rhizopus glucamylase exists in multiple forms, Gluc 1, Gluc 2, and Gluc 3, a
and degrade raw starch.
C;Genetics:
A;Intron: 51/3; 110/3; 129/1; 436/3
C;Superfamily: Rhizopus glucan 1,4-alpha-glucosidase; glucan 1,4-alpha-glucosidase homolog
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;2+5/Domain: signal sequence #status predicted <SIG>
F;26604/Product: glucan 1,4-alpha-glucosidase (Gluc 1) #status predicted <GL1>
F;34138/Domain: glucamylase starch-binding domain homology <SBP>
F;116-604/Product: (or 110-604) glucan 1,4-alpha-glucosidase (Gluc 3) #status predicted <GL2>
F;166-592/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
Query Match 26.1%; Score 724; DB 1; Length 604;
Best Local Similarity 36.8%; Pred. No. 5e-41;
Matches 165; Conservative 71; Mismatches 170; Indels 42; Gaps 10;
QY 25 ATLDSWLSNEATVARTAILNIGADGAWSGADSGIVVASPSTNDPYFTWTRDGLVL 84
Db 168 STISSWIKKQEGISRFAMLRINP----POSSATGFIASLSTAGDPYYIWTROALTS 222
QY 85 KULUDFLR--NGDTSLISTENIYSAQIYGISUPSGDSSGAGIGPERFENDEAYT 141
Db 223 NIVVYEVNTTISGNKNTILNVLYDQVYPSVKQSTSTCVN----CLGEPKPNPDCSGYT 276
QY 142 GSWGRPFODGPALARATAMIGFG-QWLIDNGTSTATIDIWPLVRNDLISYYAQWNQTYD 200
Db 277 GAMGRPONGPGERATIFLFDSDYIQTOKTOSAVYGTIKAFKOLDYVWVNWNGCFD 336
QY 201 IWEEWNGSSFFTAVORALLEGSATAVVE--CSWCDSOAPELICLQYQSFWMTCFSIL 258
Db 337 1NWEVBINGVHFTIMVWRKGILGADFAKRNGDSTRASTYSSTAAANKISSFWVSNW 396
QY 259 ANFDS----SRSKDANTU--IGSIHTFPREACDDTFOPSPRALAHKEVDS 308
Db 397 IQVSQSVTGGVSKKGJLVDVSTLIAANLGSV----DDCFFPTGSEKLUATAVEDS 447
QY 309 PRSIYLTNDGSDSEAVAVGRYPEDY----YNGNPWFLCTLAABEQLYQDVKQ 363
Db 448 FASLPYINKNLPSYLNISIGXPDETYNGNNSQGISMFLAVTGAELEYRAKING 507
QY 364 SLEUTVDSLDFKALYSDAAGT-TYSSSSSTYSSIVDAVKPFDGVSIVTHAASNMSM 422
Db 508 GVTVSSISLPPFKFDSSATSKCKYTGVTSDFNLLAQNIALAADRFLISTVQLAHNGSL 567
QY 423 SQYDSDGEGLSARDLTWSMALLTAN 450
Db 568 AEEFRDRITGGLSGARDLTWSHASLITAS 595

RESULT 13
A54549
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: 1,4-alpha-D-glucan glucohydrolase; glucoamylase
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 02-Jun-2003
C;Accession: A45499; S14396
R;Horinova, E.; Balanova, J.; Gasperik, J.
PEMS Microbiol. Lett. 67, 103-108, 1991
A;Title: the nucleotide sequence of the glucamylase gene GLA1 from *Saccharomyces* f
A;Reference number: A54549; MUID:92137640; PMID:1840532
A;Accession: A45499
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-519 <HOS>
A;Experimental source: KZ
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:78827, NCBIPI:78828)
R;Horinova, E.; Gasperik, J.
Submitted to the EMBL Data Library, March 1991
A;Description: Nucleotide and deduced amino acid sequence of the glucamylase gene from

A;Reference number: S14596
A;Accession: S14596
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-271; T⁺; 273-519 <HO2>
A;Cross-references: EMBL:X58117
C;Genetics:
A;Gene: GLA1
C;Superfamily: glucan 1,4-alpha-glucosidase; hydrolase; polysaccharide degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;41-506/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
Query Match 24.4%; Score 676.5; DB 1; Length 519;
Best Local Similarity 36.1%; Pred. No. 6.4e-38;
Matches 175; Conservative 71; Mismatches 176; Indels 63; Gaps 16;
QY 24 RATLDSWLSNEATVARTAILNIGADGAWSGADSGIVVASPSTNDPYFTWTRDGL- 82
Db 42 RTDLETFPLDKOKDVKDSVLYLQNLIAVPEGQRNDGVPGTIVASPSTSNPDYTYQWTRDASIR 101
QY 83 --VUKTLVLFNRNEDTSLISLTIENIYSAQIYGISUPSGDSSGAGIGPERFENDEAYT 137
Db 160 SAYTGAWGRPONGPALARATVAVYGTIKAFKOLDYVWVNWNGCFD 218
Db 102 FLTVLSELED--NNENTTLAKAVEYYINTSYNLORTSINPSGSFDDENHKLGEPKFNPTDG 159
QY 185 NDLSYYAQYQNTGTDIWEEWNGSSFFTAVORHALVEGSAFATV----GSSCWCD 238
Db 219 PDLEYVIGYMWSTGFDLWEENQGRHFTSLVQKAL---AYAVDIAKSFRDDGDRASYLD 274
QY 239 SQAPELICLQYQSFWMTCFSIL 288
Db 275 STASLTSYLSGSDCGFPTVNTDVH1VNPDLQONSQRLSDSATVIGPLLHD-1GESS 333
QY 289 STFQPCSPRALAHKEVDSFRSIYLTNDGLSDSEAVAVGRYPEDY----YNGNPWFL 343
Db 334 TPFDVNEVYLQSYVILLENMKDRYVSNSVY-SAGAAGRYPELVNGDGSSECNPWF 391
QY 344 CTLANABEQLDALYQMDKQSSLVEVT--DVSIDFFKALYSDAAT-----GTYSSS 391
Db 392 ATAYAQNPVKLVND-AKSASNDITNTKINYDFFKVKYIQLSITNSGYQSSDVIKGS 450
QY 392 STYSSIVDAVKPFDGVSIVTHAASNMSMSEQDKSICQELSARDLTMWSYALLTANN 451
Db 451 DEFNTVADNLVTFGDSFLQYLDHINDDSLNEOLNRTGYSTSAYSLTWSSGALLEAIR 510
QY 452 RRNSV 456
Db 511 LRNKV 515

RESULT 14
S48474
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) SCA1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: glucoamylase; protein YIL099w
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 02-Jun-2003
C;Accession: S48474; C26077; S27294
R;Bowman, S.; Churcher, C.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48455
A;Accession: S48474
A;Molecule type: DNA
A;Residues: 1-549 <HO2>
A;Cross-references: GB:247047; EMBL:238125; MUID:9603997; PID:9763247; GSFPDB:GN00009; MIP
R;Yamashita, T.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STA1
A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: C26877
A;Molecule type: DNA

A;Residues: 1-503, 507, 'W', '513-514, 'TG', '515 <YAM>
 A;Cross-references: EMBL:MI6166; NID:GI7252; PIDN:AAA35042.1; PID:GI172593
 R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
 PDBS Left: 239, 179-184, 1989
 A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Saccharomyces cerevisiae
 A;Reference number: S27284
 A;Accession: S27281; MUID:89031230; PMID:314113
 A;Molecule type: DNA
 A;Residues: 1-183, 'H', 185-190 <PAR>
 A;Cross-references: EMBL:X13858; NID:94461; PIDN:CAA32071.1; PID:94463
 C;Genetics: SGD:SGA1; MIPS:YIL099w
 A;Gene: SGD:SGA1; MIPS:YIL099w
 A;Map position: 9L
 C;Function:
 A;Description: hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from the non-reducing end of branched chains of homopolysaccharides.
 C;Superfamily: glucan 1,4-alpha-glucosidase, Yeast type; glucan 1,4-alpha-glucosidase
 C;Keywords: glycosidase; hydrolase; polysaccharide degradation; yeast vacuole
 F;77-536/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 Query Match 21.5%; Score 597; DB 1; Length 549;
 Best Local Similarity 30.4%; Pred. No. 1-6e-32;
 Matches 153; Conservative 89; Mismatches 202; Indels 60; Gaps 14;
 Qy 1 MSFSSLALSGLVCTGLANVISKRATDLSWLNRAVARTAAILNNIGADGAWNSGADSGI 60
 Db 56 VQLRDAVLMLNGTIVVYD-SNGAWDSALLEWLQGKOKVSIEKIFENIGPSAVYPS-ISPGV 113
 Qy 61 WASSTDMPDFYFWTRSGVLKTLDFRNGDTSLISTENYISQAIVQOISNSG 120
 Db 114 VIASPSQTHPDYFQWIRDSLALTINSIVS--HSAGPAIETLUQYLNVSFHLSRN-- 157
 Qy 121 DLSSGAG----LGEPKENUDETAYTGSWGRFORDGALLRATAMIGFGQQMLDNG-- 170
 Db 168 TLGAGIGYITNDTVLVALGDKPNKNDVTAFTEDWGRPQNDGPALARSTALKIIDYIKQSGTD 227
 Qy 171 ----YSTATDIWPLVRLDLSVVAQYWNQTGDIWEEVNGSSRFITIAVORHALVESSA 225
 Db 228 GAKVPPQSTA-DIFDDIVRLRFIDHMNSGFDLWEEVNGMFHFTLVLQLSAVDKSLS 286
 Qy 226 FATAVGSSCSWC---SQAEPELICV---QSPWFGSFLANF-----DSSRGDA 270
 Db 287 YFNASERSSPFVEELRQTRRDISKFVLDRANGFINGKY--NYIVGTPMIDTLSGDI 343
 Qy 271 NTLIGSIHTPDEAACDDSTFQCPSPRALANKHEVVDSDRSRISYTINDGSDSEAVGRY 330
 Db 344 STLLAANTVHDAPS-A-SHLPDFINDPAVNLTHMLHRSIYPINDSSKNAKGIALGRY 402
 Qy 331 PEDTY----YNGNPWFCLTAAABQLYQMDKQGSLEVTDVSLDFKALYSDAATG 385
 Db 403 PEDVVDGYGFEGEKGPNWVLATCTASTLYQLYRHRHSEQHDLVLPWNNDCSNAFWSELVFS 462
 Qy 386 TYSS-----SSTYSSIVDARKVTFADGVSVTETHAASNGSNSSEQVQKSDGQ 433
 Db 463 NLTTLGNDEGYLILEFNTPAFQNTIQKIFOLADSFLVLUKKAHVGDGELSEQFNKYTFGM 522
 Qy 434 LSARDITLWSYALLTANNRRNSV 457
 Db 523 QGAQHILTWSYTFMDAYQIROEVL 546
 RESULT 15
 ALBYG
 glucan 1,4-alpha-glucosidase (EC 3.2.1.3) precursor - yeast (Saccharomyces cerevisiae)
 N;Alternative names: 1,4-alpha-D-glucan glucohydrolase; glucoamylase
 C;Species: Saccharomyces cerevisiae
 C;Accession: A21896; A23470
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 05-Sep-1997
 R;Yamashita, I.; Suzuki, K.; Fukui, S.
 J;Bacteriol, 161, 567-573, 1985
 A;Title: Nucleotide sequence of the extracellular glucamylase gene STA1 in the yeast S. cerevisiae
 A;Reference number: A21896; MUID:85104778; PMID:3918017
 A;Note: S. diastaticus

A;Accession: A21896
 A;Molecule type: DNA
 A;Residues: 1-178 <YAL>
 A;Experimental source: strain S106-9A; ATCC 60709
 R;Yamashita, I.; Suzuki, K.; Sakizo, F.
 Agric. Biol. Chem. 50, 475-482, 1986
 A;Title: Proteolytic processing of glucoamylase in the yeast Saccharomyces cerevisiae.
 A;Reference number: A23470
 A;Contents: signal sequence cleavage site
 A;accession: A23470
 A;Molecule type: protein
 A;Residues: 1-65 <YAL>
 C;genetics:
 A;Gene: STA1
 C;Superfamily: yeast glucan 1,4-alpha-glucosidase STA1; glucan 1,4-alpha-glucosidase homeologous genes
 C;Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; polysaccharide catabolism
 F;1-32/Domain: signal sequence #status experimental <SIG>
 F;33-778/Product: glucan 1,4-alpha-glucosidase #status predicted <MP>>
 F;345-778/Domain: glucan 1,4-alpha-glucosidase homology <GAG>
 F;6,319,333,425,434,445,54,55,65,661,731,752/Binding site: carbohydrate (Asn) (covalent)
 F;635/Active site: Asp #status predicted
 Query Match 18.8%; Score 522; DB 1; Length 778;
 Best Local Similarity 30.5%; Pred. No. 2.8e-27;
 Matches 139; Conservative 80; Mismatches 177; Indels 60; Gaps 15;
 Qy 1 MSFSSLALSGLVCTGLANVISKRATDLSWLNRAVARTAAILNNIGADGAWNSGADSGI 60
 Db 324 VQLRDAVLMLNGTIVVYD-SNGAWDSALLEWLQGKOKVSIEKIFENIGPSAVYPS-ILPGV 381
 Qy 61 VVASPSTNDPFDYFTWTDGLVLTFLDFRNGDTSLISTENYISQAIVQOISNSG 120
 Db 382 VIASPSQTHPDYFQWIRDSLALTINSIVS--HSADPAIETLUQYLNVSFHLSRN-- 435
 Qy 121 DLSSGAG----LGEPKENUDETAYTGSWGRFORDGALLRATAMIGFGQQMLDNG-- 170
 Db 121 DLSSGAG----LGEPKENUDETAYTGSWGRFORDGALLRATAMIGFGQQMLDNG-- 170
 Qy 436 TLGAGIGYITNDTVLVALGDKPNKNDVTAFTEDWGRPQNDGPALARSTALKIIDYIKQSGTD 495
 Qy 171 ----YSTATDIWPLVRLDLSVVAQYWNQTGDIWEEVNGSSRFITIAVORHALVESSA 225
 Db 496 GAKVPPQSTA-DIFDDIVRLRFIDHMNSGFDLWEEVNGMFHFTLVLQLSAVDRSL 554
 Db 226 FATAVGSSCSWC---SQAEPELICV---QSPWFGSFLANF-----DSSRGDA 270
 Db 555 YFNASERSSPFVEELRQTRRDISKFVLDRANGFINGKY--NYIVGTPMIDTLSGDI 611
 Qy 271 NTLIGSIHTPDEAACDDSTFQCPSPRALANKHEVVDSDRSRISYTINDGSDSEAVGRY 330
 Db 612 STLLAANTVHDAPS-A-SHLPDFINDPAVNLTHMLHRSIYPINDSSKNAKGIALGRY 670
 Qy 331 PEDTY----YNGNPWFCLTAAABQLYQMDKQGSLEVTDVSLDFKALYSDAATG 385
 Db 671 PEDVVDGYGFEGEKGPNWVLATCTASTLYQLYRHRHSEQHDLVLPWNNDCSNAFWSELVFS 730
 Qy 386 TYSS-----SSTYSSIVDARKVTFADGVSVTETHAASNGSNSSEQVQKSDGQ 409
 Db 731 NLTTLGNDEGYLILEFNTPAFQNTIQKIFOLADSFLVLUKKAHVGDGELSEQFNKYTFGM 522
 Search completed: June 17, 2004, 17:48:00
 Job time : 22 sec

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OM protein - protein search, using SW model
Run on: June 17, 2004, 17:35:48 ; Search time 59 Seconds
(without alignments)
2557.294 Million cell updates/sec

Title: US-10-038-723-2

Perfect score: 2771

Sequence: 1 MSFRSLIALSGLVCTGIANV.....SKTTATASAKTSTTRSGMSL 534

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:**

1: geneseqP1980s:**
2: geneseqP1990s:**
3: geneseqP2000s:**
4: geneseqP2001s:**
5: geneseqP2002s:**
6: geneseqP2003as:**
7: geneseqP2003bs:**
8: geneseqP2004s:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2771	100.0	534 2	AAY18090 Truncated Aay18090 Aspergillus
2	2771	100.0	534 2	AAY23338 Truncated Aay23338 Aspergillus
3	2771	100.0	534 3	Aab03450 Aspergillus
4	2771	100.0	534 3	Aay7740 A. niger
5	2771	100.0	534 4	Aab48171 A. niger
6	2771	100.0	534 4	Aab61904 A. niger
7	2742	99.0	640 3	Aay7741 A. niger
8	2742	99.0	640 4	Aab61905 A. niger
9	2683.5	96.8	639 1	Aap40212 Sequence
10	2658	95.9	630 1	Aap81876 Sequence
11	2628	94.8	616 3	AB15176 Aspergillus
12	2625	94.7	616 2	Aay5979 Aspergillus
13	2625	94.7	616 3	AB15180 Aspergillus
14	2615	94.4	616 2	Aaw55976 Aspergillus
15	2615	94.3	616 3	AB15178 Aspergillus
16	2614	94.3	616 3	AB15184 Aspergillus
17	2612	94.3	616 3	AB15181 Aspergillus
18	2612	94.3	616 3	AB15182 Aspergillus
19	2604	94.0	616 2	Aaw55977 Aspergillus
20	2604	94.0	616 3	AB15179 Aspergillus
21	2600.5	93.8	621 2	Aaw55978 Aspergillus
22	2589.5	93.5	621 3	AB15183 Aspergillus
23	2584.5	93.3	621 3	AB15182 A. awamori
24	2523	91.1	1095 4	ABp96330 Alpha-amylase
25	2468	89.1	471 4	Abm00045 AMG SEQ I

ALIGNMENTS

26	1850.5	66.8	631 6	ABB80181 A. fumiga
27	1770	63.9	624 4	Aab48170 Thermobac
28	1689	61.4	581 5	Aay23339 Talaromyces
29	1674.5	60.4	591 2	Aay23337 Talaromyces
30	1615.5	58.3	630 5	Aam51596 Thielavia
31	1577	56.9	626 2	Aar71034 N. crassa
32	1425.5	51.4	581 3	Aab18823 Amino aci
33	1425.5	51.4	581 5	Aau79444 Fusarium
34	1425.5	51.4	581 7	Abp01925 Fusarium
35	1408.5	50.8	704 6	Abb80170 A. fumiga
36	1380.5	49.8	620 6	Abb80174 A. fumiga
37	1321	47.7	616 2	Aaw30155 Glucoamyl
38	725	26.2	579 6	Abp96332 Rhizopus
39	724	26.1	604 1	Aap60359 Glucoamyl
40	641.5	23.2	624 2	Aar77674 Glucoamyl
41	615.5	22.2	497 1	Aap70572 Glucoamyl
42	600.5	21.7	918 1	Aap60723 Sequence
43	374	29.3	1 1	Aap70183 Sequence
44	181	6.5	1588 7	Adc01413 Enterohe
45	172	6.2	2 2	Aar22343 His(184)

This sequence is a truncated A. niger glucoamylase G1 protein. The invention relates to a method of saccharifying a liquefied starch solution comprising: (a) a saccharification step during which one or more enzymatic saccharification stages (using a mutated Aspergillus niger Aaw55978 Aspergillus) take place; (b) one or more high temperature membrane separation steps; and (c) re-circulation of the saccharification enzyme, in which the membrane separation steps are carried out as an integral part of the saccharification step. The method can be used for the production of mono and/or oligosaccharides from starch, including

CC	dextrose; trehalose; isomaltooligosaccharides, cyclodextrins or maltoligosaccharides. The use of the membrane separation step improves the efficiency of the process and improves yields and purity
XX	Sequence 534 AA;
PA	Query Match 100.0%; Score 2771; DB 2; Length 534; Best Local Similarity 100.0%; Pred. No. 1.5e-214; Mismatches 0; Indels 0; Gaps 0;
XX	Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PI	QY 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
XX	Db 61 WVASPSTNDPDPYFTWTRDGLVLUKTLVLDFRNGDTSLISTIENIQAIVQGSNPG 120 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
DR	QY 61 WVASPSTNDPDPYFTWTRDGLVLUKTLVLDFRNGDTSLISTIENIQAIVQGSNPG 120 61 WVASPSTNDPDPYFTWTRDGLVLUKTLVLDFRNGDTSLISTIENIQAIVQGSNPG 120
XX	Db 121 DLSSGAGLGEPKENDEATGWSWRPQRDGPAKRATAMIGFGQWILDNGTSTATDIW 180 121 DLSSGAGLGEPKENDEATGWSWRPQRDGPAKRATAMIGFGQWILDNGTSTATDIW 180
PT	QY 121 DLSSGAGLGEPKENDEATGWSWRPQRDGPAKRATAMIGFGQWILDNGTSTATDIW 180 Db 181 PLVRNDLSYVAQYWNQTYGDLWEVNGSSFTIAVQRHALVEGSAFATAVGSSCNSCDQ 240 181 PLVRNDLSYVAQYWNQTYGDLWEVNGSSFTIAVQRHALVEGSAFATAVGSSCNSCDQ 240
XX	Db 241 APEILCYLQSFWTSFPLIANFDSSRSRKDANTLISIHTPDEAACDDSTFOPCSRALA 300 241 APEILCYLQSFWTSFPLIANFDSSRSRKDANTLISIHTPDEAACDDSTFOPCSRALA 300
PS	QY 301 NHKEVUDSPRSIYTFLNDGLDSEAVAVGRYPEDTYINGNPFLCTLAABQLYQWD 360 301 NHKEVUDSPRSIYTFLNDGLDSEAVAVGRYPEDTYINGNPFLCTLAABQLYQWD 360
XX	Db 361 KQGSLEVTDSLDFKALYSDAATGTYSSSSTSYSSITDVAKTFADGFVSIVETHASNG 420 361 KQGSLEVTDSLDFKALYSDAATGTYSSSSTSYSSITDVAKTFADGFVSIVETHASNG 420
CC	QY 421 SMSEQYDKSDGEQLSARDLTVSYALLTANRNRSVPASNGETASSVPGTCATSAG 480 421 SMSEQYDKSDGEQLSARDLTVSYALLTANRNRSVPASNGETASSVPGTCATSAG 480
CC	Db 481 TYSSTVTSPSPIVATGGTTTATPTGGSYTSKTTASKSTTTRSGMSL 534 481 TYSSTVTSPSPIVATGGTTTATPTGGSYTSKTTASKSTTTRSGMSL 534
CC	Db 481 TYSSTVTSPSPIVATGGTTTATPTGGSYTSKTTASKSTTTRSGMSL 534
XX	Db RESULT 2 AAY23338 standard; protein; 534 AA.
CC	Db AAY23338; ID 02-SEP-1999 (first entry)
XX	DE Aspergillus niger glucoamylase enzyme.
XX	KW Glucoamylase enzyme; saccharification; starch hydrolysate; dextrose syrup; syrup; ethanol; fuel; beverage; citric acid; ascorbic acid; lysine; glutamic acid.
XX	OS Aspergillus niger.
XX	PN W0928448-A1.
XX	PD 10-JUN-1999.
PR	PF 26-NOV-1998; 98WO-DK00520.
PR	PR 26-NOV-1997; 97US-00979673.
PR	30-DEC-1997; 97D5-0001557.
PR	30-JUN-1998; 98US-0017657.
PR	10-JUL-1998; 98DK-0000925.
XX	RESULT 3 AAB03450
XX	ID AAB03450 standard; protein; 534 AA.
AC	AAB03450;
XX	AC
PA	(NOVO) NOVO-NORDISK AS.
XX	WPI; 1999-404822/34.
DR	N-PSDB; AX1797.
XX	New glucomylase obtained from Talaromyces emersonii.
PS	Disclosure; Page 63-64; 79pp; English.
XX	The present sequence represents a glucomylase enzyme obtained from Aspergillus niger. The specification describes a Talaromyces emersonii glucomylase enzyme. The glucomylase enzymes have high thermal stability so that saccharification process may be carried out within a shorter period of time or the process may be carried out using a lower enzyme dosage. The glucomylase enzymes can be used for saccharifying starch hydrolylate for converting starch or partially hydrolysed starch into a syrup containing dextrose. They can be used for producing beverages or oligosaccharides, specialty syrups, ethanol for fuel, beverages or organic compounds such as citric acid, ascorbic acid, lysine or glutamic acid
XX	Sequence 534 AA;
PA	Query Match 100.0%; Score 2771; DB 2; Length 534; Best Local Similarity 100.0%; Pred. No. 1.5e-214; Mismatches 0; Indels 0; Gaps 0;
XX	Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PI	QY 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
XX	Db 61 WVASPSTNDPDPYFTWTRDGLVLUKTLVLDFRNGDTSLISTIENIQAIVQGSNPG 120 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
DR	QY 61 WVASPSTNDPDPYFTWTRDGLVLUKTLVLDFRNGDTSLISTIENIQAIVQGSNPG 120 61 WVASPSTNDPDPYFTWTRDGLVLUKTLVLDFRNGDTSLISTIENIQAIVQGSNPG 120
XX	Db 121 DLSSGAGLGEPKENDEATGWSWRPQRDGPAKRATAMIGFGQWILDNGTSTATDIW 180 121 DLSSGAGLGEPKENDEATGWSWRPQRDGPAKRATAMIGFGQWILDNGTSTATDIW 180
PT	QY 121 DLSSGAGLGEPKENDEATGWSWRPQRDGPAKRATAMIGFGQWILDNGTSTATDIW 180 Db 181 PLVRNDLSYVAQYWNQTYGDLWEVNGSSFTIAVQRHALVEGSAFATAVGSSCNSCDQ 240 181 PLVRNDLSYVAQYWNQTYGDLWEVNGSSFTIAVQRHALVEGSAFATAVGSSCNSCDQ 240
XX	Db 241 APEILCYLQSFWTSFPLIANFDSSRSRKDANTLISIHTPDEAACDDSTFOPCSRALA 300 241 APEILCYLQSFWTSFPLIANFDSSRSRKDANTLISIHTPDEAACDDSTFOPCSRALA 300
PS	QY 301 NHKEVUDSPRSIYTFLNDGLDSEAVAVGRYPEDTYINGNPFLCTLAABQLYQWD 360 301 NHKEVUDSPRSIYTFLNDGLDSEAVAVGRYPEDTYINGNPFLCTLAABQLYQWD 360
XX	Db 361 KQGSLEVTDSLDFKALYSDAATGTYSSSSTSYSSITDVAKTFADGFVSIVETHASNG 420 361 KQGSLEVTDSLDFKALYSDAATGTYSSSSTSYSSITDVAKTFADGFVSIVETHASNG 420
CC	QY 421 SMSEQYDKSDGEQLSARDLTVSYALLTANRNRSVPASNGETASSVPGTCATSAG 480 421 SMSEQYDKSDGEQLSARDLTVSYALLTANRNRSVPASNGETASSVPGTCATSAG 480
CC	Db 421 SMSEQYDKSDGEQLSARDLTVSYALLTANRNRSVPASNGETASSVPGTCATSAG 480 421 SMSEQYDKSDGEQLSARDLTVSYALLTANRNRSVPASNGETASSVPGTCATSAG 480
CC	Db 481 TYSSTVTSPSPIVATGGTTTATPTGGSYTSKTTASKSTTTRSGMSL 534 481 TYSSTVTSPSPIVATGGTTTATPTGGSYTSKTTASKSTTTRSGMSL 534
XX	Db RESULT 3 AAB03450
XX	ID AAB03450 standard; protein; 534 AA.
AC	AAB03450;
XX	AC

DT 03-JAN-2001 (first entry)
 XX DE Aspergillus niger G2 glucoamylase.
 XX KW Glucoamylase G2; starch hydrolysis; high fructose corn syrup;
 KW thermal stability.
 XX OS Aspergillus niger.
 XX FH Key Peptide
 FT Location/Qualifiers
 FT 1. :27 /label= prepropeptide_sequence
 FT 27. :28 /label= tripeptidyl_amino_peptidase_cleavage_site
 FT 28. :534 /label= mature_glucoamylase
 FT XX PN WO20034452-A1.
 XX PD 15-JUN-2000.
 XX PR 07-DEC-1999; 99WO-DK000686.
 XX PR 07-DEC-1998; 98DK-00001616.
 XX PR 24-MAR-1999; 99DK-0000409.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX Nielsen BR, Svendsen A, Bojsen K, Vind J, Pedersen H;
 PI DR WPI; 2000-43126/37.
 XX PT Variants of parent fungal glucoamylase useful for producing ethanol,
 PT beverages and in fermentation processes comprise a peptide extension at
 PT the amino terminal.
 XX Disclosure; Page 50-51; 61pp; English.
 CC The present sequence is the G2 glucoamylase from Aspergillus niger. It
 CC was used to construct a version of the enzyme which has improved thermal
 CC stability, and which can be used more efficiently in starch hydrolysis.
 CC This process is used during high fructose corn syrup production, as well
 CC as in the production of ethanol for fuel or beverage, and in fermentation
 CC processes for producing organic compounds such as citric acid, ascorbic
 CC acid, lysine and glutamic acid
 XX SQ Sequence 534 AA:
 Query Match 100 %; Score 2771; DB 3; Length 534;
 Best Local Similarity 100 %; Pred. No. 1.5e-214;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSFRSIALSLSILSVCTGLANVSKRATLDSWISNEATVARTILNNIGADGAWNSGADSGI 60
 Db 1 MSFRSIALSLSILSVCTGLANVSKRATLDSWISNEATVARTILNNIGADGAWNSGADSGI 60
 QY 61 VVASPSTDNPYFTWTRDSVLKVLTVDLFLRNGDTSLLSTENIYSAQAVOGISNPSG 120
 Db 61 VVASPSTDNPYFTWTRDSVLKVLTVDLFLRNGDTSLLSTENIYSAQAVOGISNPSG 120
 QY 121 DLSGAGLGERKFENVDETAATYGSWGRQDGPALRATAMIGRGQMLDNGTSTADIW 180
 Db 121 DLSGAGLGERKFENVDETAATYGSWGRQDGPALRATAMIGRGQMLDNGTSTADIW 180
 QY 181 PLVRNDLSYVAQIWNQTYGYDWEEWVGSSFPITIAVORALYVEGSAFATAVQSSCWDQS 240
 Db 181 PLVRNDLSYVAQIWNQTYGYDWEEWVGSSFPITIAVORALYVEGSAFATAVQSSCWDQS 240
 QY 241 APEILCYLQSFMTGSPFLANFDSSRGKDANTLIGSIHTPPEAEDDSTSOPCSRALA 300
 Db 241 APEILCYLQSFMTGSPFLANFDSSRGKDANTLIGSIHTPPEAEDDSTSOPCSRALA 300
 QY 301 NHKEVUDSFRSYTLDGLSSEAVAVGYPBDTYINGNPFLCTLAEEQLYDALYQMD 360

Db 301 NHKEVUDSFRSYTLDGLSSEAVAVGYPBDTYINGNPFLCTLAEEQLYDALYQMD 360
 QY 361 KQGSLEVDIVSLDFKKLYSDATGTYSSSSSTISSIVDAVKTFADGVSVTETHASNG 420
 Db 361 KQGSLEVDIVSLDFKKLYSDATGTYSSSSSTISSIVDAVKTFADGVSVTETHASNG 420
 QY 421 SMSEQYDKSDBEQLSARLDTWSYAAUHTANNRRNSVPASWGETSASVPGTCATSAIG 480
 Db 421 SMSEQYDKSDBEQLSARLDTWSYAAUHTANNRRNSVPASWGETSASVPGTCATSAIG 480
 QY 481 TYSVVTWSMSIVAGTTATPGSGSVTSTKATASKSITTRGMSL 534
 Db 481 TYSVVTWSMSIVAGTTATPGSGSVTSTKATASKSITTRGMSL 534

RESULT 4
 AAY77740
 ID AAY77740 Standard; protein; 534 AA.
 XX AC AAY77740;
 XX DT 22-MAY-2000 (first entry)
 XX DE A. niger G2 glucoamylase.
 XX KW Glucoamylase; variant; starch conversion; saccharification; ethanol;
 KW fuel; beverage; fermentation; citric acid; ascorbic acid; thermostable;
 KW G2 glucoamylase; fungal.
 XX OS Aspergillus niger.
 XX PN WO20004136-A1.
 XX BD 27-JAN-2000.
 XX PP 09-JUL-1999; 99WO-DK000392.
 XX PR 15-JUL-1998; 98DK-00000937.
 XX PR 17-DEC-1998; 98DK-00001667.
 XX PA (NOVO) NOVO-NORDISK AS.
 XX Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
 PI Frandsen TP;
 XX DR WPI; 2000-182412/16.
 DR N-PSB; AAZ8742.
 XX PT Variant fungal glucoamylases with improved thermostability and increased
 PT specific activity, useful in saccharification processes.
 XX BS Claim 1; Page 78-81; 116pp; English.
 CC The invention relates to variant fungal glucoamylases comprising specific
 CC mutations. The variant comprises one or more mutation in position/region
 CC 1-18, 19-35, 40-62, 73-80, 93-127, 200-212, 234-246, 287-319,
 CC 334-341, 353-374, 388-414, 445-470 of the parent G2 glucoamylase sequence
 (AAY77740) from A. niger, with the exception of N20C, A27C, S30P, Y48W,
 (AYY77740) from A. niger, with the exception of N20C, A27C, S30P, Y48W,
 CC Y50F, W52F, R54K/L, D55G, G57A, K108R, D112Y, Y116A/W, S119C/W/E/G/Y/P,
 CC W120H/L/F/Y, G121T/A, R122Y, P123G, Q124H, R125K, W170P, N171S, Q172N, CC
 CC T173G, G174C, Y175F, D176N/E, L177H/D, W178R/D, E179Q/D, E180D/Q,
 CC V181D/A/T, N182A/D/Y/S, G183K, S184H, W212P, R246C, A246C, D293E/Q,
 CC A302V, R305K, Y306F, D319N/E, Y312W, W317, E319D/Q, H319W, A319D, A319P,
 CC N319Q, G319S, B400Q/C, Q401E, G407P, L410F, S411A/G/C/H/D, and
 S460P. The glucoamylase variants are useful in a starch conversion
 CC process, especially continuous process which include a continuous
 CC saccharification process. The variants can be used for producing
 CC oligosaccharides, specialty syrups or ethanol for fuel or beverages.
 CC They can also be used in fermentation processes for producing organic
 CC compounds such as citric acid, ascorbic acid, lysine and glutamic acid.
 CC The glucoamylase variants have improved thermostability and/or increased
 CC specific activity. This is advantageous in industrial saccharification

CC processes. The risk of microbial contamination is also reduced when carrying the saccharification process at temperatures above 63 °C.

CC An increased specific activity towards short chain saccharides such as maltose (without reducing the activity toward oligosaccharides) would CC also permit using a lower enzyme dosage and/or shorter process times. The present sequence represents the G2 glucoamylase from *A. niger*, the parent CC glucoamylase used for constructing the variants

XX SQ Sequence 534 AA:
 Query Match 100.0%; Score 2771; DB 3; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1.5e-214; Mismatches 0; Indels 0; Gaps 0;
 Matches 534; Conservative 0; N mismatches 0; DR DR
 Db 1 MSFRSLLAISGLVCTGLANVSKRATLDSMSLNESATVARTAILNNIGADGAWNSGADSGI 60
 QY 1 MSFRSLLAISGLVCTGLANVSKRATLDSMSLNESATVARTAILNNIGADGAWNSGADSGI 60
 Db 61 VVASPSTDNPDYFTWTRDGLVIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120
 QY 61 VVASPSTDNPDYFTWTRDGLVIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120
 Db 121 DLSSGAGI GEPKENVDEATYGSNQRPQDGPA RATA MIGFGQWL DINGYSTATDIW 180
 QY 121 DLSSGAGI GEPKENVDEATYGSNQRPQDGPA RATA MIGFGQWL DINGYSTATDIW 180
 Db 181 PLVRNDLSVVAQYMNQQTGDW LWE E VNG SFTIAVQHRA LVE GSA F A TAVG SCSW CDSQ 240
 QY 181 PLVRNDLSVVAQYMNQQTGDW LWE E VNG SFTIAVQHRA LVE GSA F A TAVG SCSW CDSQ 240
 Db 181 PLVRNDLSVVAQYMNQQTGDW LWE E VNG SFTIAVQHRA LVE GSA F A TAVG SCSW CDSQ 240
 QY 241 APETI CYLQSF WTGSF PI LANFDSSRSKG DANT LGS IHT FPEACD STFQ PCSP RAL A 300
 Db 241 APETI CYLQSF WTGSF PI LANFDSSRSKG DANT LGS IHT FPEACD STFQ PCSP RAL A 300
 QY 301 NHKEVUDSRSI YVTLNDGLSDSEAV A VGR Y P E D T Y G N P W F U C T L A A E Q L D A Y Q D 360
 Db 301 NHKEVUDSRSI YVTLNDGLSDSEAV A VGR Y P E D T Y G N P W F U C T L A A E Q L D A Y Q D 360
 QY 361 KQGSLE VT D V S D F K A L Y S D A A G T Y S S S T V S S I V D A V K I F A D G F V S I V E H A S N G 420
 Db 361 KQGSLE VT D V S D F K A L Y S D A A G T Y S S S T V S S I V D A V K I F A D G F V S I V E H A S N G 420
 QY 421 SMSEQYDKSDGEQLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480
 Db 421 SMSEQYDKSDGEQLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480
 QY 481 TYSSVTVTSWPSIVATGGTTATPTGS S V T S K T T A T S K T I T R S G M S L 534
 Db 481 TYSSVTVTSWPSIVATGGTTATPTGS S V T S K T T A T S K T I T R S G M S L 534
 RESULT 5
 AAB48171 ID AAB48171 standard; protein; 534 AA.
 XX AC AAB48171;
 XX DT 02-APR-2001 (first entry)
 DE A. niger Glucoamylase polypeptide.
 XX KW Thermoascus crustaceus; glucoamylase; starch conversion; ethanol; KW maltose syrup; beverage; citric acid; ascorbic acid; detergent; KW thermostability; glucose; Glucoamylase.
 XX OS Aspergillus niger.
 XX FH Key location/Qualifiers
 FT Peptide 1.-24 /note= "Signal peptide"
 FT Protein 25.-534 /note= "mature protein"
 XX

PN WO200075296-A1.

XX PD 14-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-DK000301.
 XX PR 02-JUN-1999; 99DK-00000779.

XX PA (NOVO) NOVO NORDISK AS.

XX PI Nielsen BR, Kauppinen MS, Nielsen RI;

XX DR WPI; 2001-071066/08.
 N-PSDB; AACB444.

XX Novel Thermascus crustaceus glucoamylase polypeptide useful in a PT continuous starch conversion process, detergents and for producing PT oligosaccharides, specialty syrups, ethanol for fuel or drinking, and PT beverages.
 XX Disclosure; Page 52-55; 61pp; English.
 CC The invention provides a Thermascus crustaceus glucoamylase polypeptide. CC The glucoamylase polypeptide can be expressed by standard recombinant methodology and is useful in a continuous starch conversion process, for CC producing oligosaccharides, specialty syrups such as maltose syrups, CC ethanol for fuel or drinking, ethanol, beverages, and organic compounds CC such as citric acid, ascorbic acid, lysine or glutamic acid. It is also CC useful in detergents, such as laundry detergent compositions, dish wash compositions and/or hard surface cleaning compositions. The *T. crustaceus* CC glucoamylase has higher thermostability than *Aspergillus niger* G1 CC glucoamylase. It also has higher specific activity and/or decreased CC glucose reversion tendency. The present sequence represents the *A. niger* G1 glucoamylase.

XX SQ Sequence 534 AA:
 Query Match 100.0%; Score 2771; DB 4; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1.5e-214; Mismatches 0; Indels 0; Gaps 0;
 Matches 534; Conservative 0; N mismatches 0; DR DR
 Db 1 MSFRSLLAISGLVCTGLANVSKRATLDSMSLNESATVARTAILNNIGADGAWNSGADSGI 60
 QY 1 MSFRSLLAISGLVCTGLANVSKRATLDSMSLNESATVARTAILNNIGADGAWNSGADSGI 60
 Db 61 VVASPSTDNPDYFTWTRDGLVIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120
 QY 61 VVASPSTDNPDYFTWTRDGLVIKTLVLDLFRNGDTSLISTENYISQAIVOGISNSG 120
 Db 121 DLSSGAGI GEPKENVDEATYGSNQRPQDGPA RATA MIGFGQWL DINGYSTATDIW 180
 QY 121 DLSSGAGI GEPKENVDEATYGSNQRPQDGPA RATA MIGFGQWL DINGYSTATDIW 180
 Db 181 PLVRNDLSVVAQYMNQQTGDW LWE E VNG SFTIAVQHRA LVE GSA F A TAVG SCSW CDSQ 240
 QY 181 PLVRNDLSVVAQYMNQQTGDW LWE E VNG SFTIAVQHRA LVE GSA F A TAVG SCSW CDSQ 240
 Db 241 APETI CYLQSF WTGSF PI LANFDSSRSKG DANT LGS IHT FPEACD STFQ PCSP RAL A 300
 QY 241 APETI CYLQSF WTGSF PI LANFDSSRSKG DANT LGS IHT FPEACD STFQ PCSP RAL A 300
 Db 301 NHKEVUDSRSI YVTLNDGLSDSEAV A VGR Y P E D T Y G N P W F U C T L A A E Q L D A Y Q D 360
 QY 301 NHKEVUDSRSI YVTLNDGLSDSEAV A VGR Y P E D T Y G N P W F U C T L A A E Q L D A Y Q D 360
 Db 361 KQGSLE VT D V S D F K A L Y S D A A G T Y S S S T V S S I V D A V K I F A D G F V S I V E H A S N G 420
 QY 421 SMSEQYDKSDGEQLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480
 Db 421 SMSEQYDKSDGEQLSARDLTWSYALLTANNRNSVUPASWGETSASSVPGTCATSAIG 480

QY 481 TSSVTWPSIVATGGTTATPGSGSVTISKTTASKSTTTRGMSL 534
 Db 481 TYSSVTWPSIVATGGTTATPGSGSVTISKTTASKSTTTRGMSL 534

RESULT 6

AAB61904
 ID AAB61904 standard; protein; 534 AA.
 AC AAB61904;
 XX
 DT 08-MAY-2001 (first entry)
 DE A. niger G2 glucoamylase.
 KW Glucoamylase; variant; starch; dextrose; saccharification; maltodextrin; glucose syrup; fuel; ethanol; beverage; fermentation; citric acid; ascorbic acid.
 XX
 OS Aspergillus niger.

PH Key Location/Qualifiers
 PT Peptide 1..24
 FT Protein /note= "signal peptide"
 FT 25..534 /note= "mature protein"

XX WO200104273-A2.
 XX PD 18-JAN-2001.
 XX PP 07-JUL-2000; 2000WO-DK000373.
 XX PR 09-JUL-1999; 99DK-00000999.
 XX PA (NOVO) NOVO NORDISK AS.
 XX PI Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
 PI Frandsen TP;
 XX WPI; 2001-138334/14.
 DR N-PSDB; AAC85099.

XX Novel variant of parent glucoamylase useful in starch conversion process, and for producing oligosaccharides, malodextrins, glucose syrups, fuel, drinking ethanol, beverage and organic compounds.

XX Claim 1; Page 51-53; 58pp; English.

The invention relates to a variant of a parent glucoamylase, comprising an alteration at positions 59, 66, 72, 119, 189, 223, 313, 340, 342, 352, 373, 386, 393, 395, 402, 408, 416, 425, 427, 444, 486, 490, 494, where the alteration is independently an insertion, substitution or deletion of amino acid which occupies the position. The variant glucoamylase is useful for converting starch or partially hydrolyzed starch into a syrup containing dextrose, by saccharifying starch hydrolyzate. The variant is useful in the starch conversion process, for producing oligosaccharides, malodextrins or glucose syrups, fuel, drinking ethanol, beverage and in a fermentation process for producing organic compounds, such as citric acid, ascorbic acid, lysine and glutamic acid. It is useful for improving the thermal stability and/or specific activity of a parent glucoamylase. The present sequence represents an A. niger G2 glucoamylase, the parent enzyme from which the variant of the invention is derived

XX Sequence 534 AA;

Query Match 100.0%; Score 2771; DB 4; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1..5e-214; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFRSLIALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGDAGAWVGADSGI 60
 Db 61 VVASPSTDNPYFTWTRDSGLVKTLDLFRNGTTSLSIENYISQAIVQGTSNPG 120
 Qy 61 VVASPSTDNPYFTWTRDSGLVKTLDLFRNGTTSLSIENYISQAIVQGTSNPG 120

RESULT 7

AY77741
 ID AY77741 standard; protein; 640 AA.
 AC AY77741;
 XX
 DT 22-MAY-2000 (first entry)
 DE A. niger G1 glucoamylase.
 XX Glucoamylase; variant; starch conversion; saccharification; ethanol; fuel; beverage; fermentation; citric acid; ascorbic acid; thermostable; G1 glucoamylase; fungal.

XX Aspergillus niger.

XX WO20004136-A1.

XX PD 27-JAN-2000.

PP 09-JUN-1999; 99WO-DK000392.

PR 15-JUL-1998; 98DK-00000937.

BR 17-DEC-1998; 98DK-0001667.

XX (NOVO) NOVO-NORDISK AS.

XX Nielsen BR, Svendsen A, Pedersen H, Vind J, Hendriksen HV;
 PI Frandsen TP;
 XX N-PSDB; AAC287843.

DR WPI; 2000-182412/16.

XX Variant fungal glucoamylases with improved thermostability and increased PT specific activity, useful in saccharification processes.

XX Disclosure; Page 91-93; 116pp; English.

Query Match 1 MSFRSLIALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGDAGAWVGADSGI 60
 Best Local Similarity 100.0%; Pred. No. 1..5e-214; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFRSLIALSGLVCTGLANVSKRATLDSWLSNEATVARTAILNNIGDAGAWVGADSGI 60

CC The invention relates to variant fungal glucoamylases. The variants
 CC comprise specific mutations in the parent G2 glucoamylase (AMG) sequence
 CC (AAV77740) from *A. niger* (see AAV87842 for specific positions of the
 CC mutations). The glucoamylase variants are useful in a starch conversion
 CC process, especially continuous process which include a continuous
 CC saccharification process. The variants can be used for producing
 CC oligosaccharides, specialty syrups, or ethanol for fuel or beverages.
 CC They can also be used in fermentation processes for producing organic
 CC compounds such as citric acid, ascorbic acid, lysine and glutamic acid.
 CC The glucoamylase variants have improved thermostability and/or increased
 CC specific activity. This is advantageous in industrial saccharification
 CC process. The risk of microbial contamination is also reduced when
 CC carrying the saccharification process at temperatures above 63 $^{\circ}$ C. An
 CC increased specific activity towards short chain saccharides such as
 CC maltose (without reducing the activity towards oligosaccharides) would
 CC also permit using a lower enzyme dosage and/or shorter process times. The
 CC present sequence represents the GI glucoamylase from *A. niger*

XX Sequence 640 AA;

Query Match 99.0%; Score 2742; DB 3; Length 640;
 Best Local Similarity 99.6%; Pred. No. 4.4e-212; No. of
 Matches 528; Conservative 1; MisMatches 1; Indels 0; Gaps 0;

QY 1 MSFRSIALSGLVCTGLANVISKRATLDSMSLNBEATVARTAILNNIGAWGAWSGADSGI 60
 1 MSFRSIALSGLVCTGLANVISKRATLDSMSLNBEATVARTAILNNIGAWGAWSGADSGI 60

QY 61 WVASPTNDPYFTWTRDGLVLTLDLFRNGDTSLISTIENYISAQIVOGISINPSG 120
 61 WVASPTNDPYFTWTRDGLVLTLDLFRNGDTSLISTIENYISAQIVOGISINPSG 120

Db 121 DLSSGAGLGPKFKNDEATYGSGWGRPDRGPAKRALATAMIGFGQMLLDNGYTSTATDW 180
 121 DLSSGAGLGPKFKNDEATYGSGWGRPDRGPAKRALATAMIGFGQMLLDNGYTSTATDW 180

QY 181 PLVRNDLSVVAQYMNQTYGDLWEENGSSFTIAVQHRAVEGSAFATAVGSSCSWCDSQ 240
 181 PLVRNDLSVVAQYMNQTYGDLWEENGSSFTIAVQHRAVEGSAFATAVGSSCSWCDSQ 240

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300
 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360
 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420
 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 421 SMSBQDKSDGEQSLARDLWMSYALLTANRNRNSVUPASWGETSASSVPGTCATSAIG 480
 421 SMSBQDKSDGEQSLARDLWMSYALLTANRNRNSVUPASWGETSASSVPGTCATSAIG 480

QY 481 TYSSTVTSSPSIVATGGTTATGTGSVGVTSISKTTASKTITRS 530
 481 TYSSTVTSSPSIVATGGTTATGTGSVGVTSISKTTASKTITRS 530

Db 181 PLVRNDLSVVAQYMNQTYGDLWEENGSSFTIAVQHRAVEGSAFATAVGSSCSWCDSQ 240
 181 PLVRNDLSVVAQYMNQTYGDLWEENGSSFTIAVQHRAVEGSAFATAVGSSCSWCDSQ 240

SQ Sequence 640 AA;

Query Match 99.0%; Score 2742; DB 4; Length 640;
 Best Local Similarity 99.6%; Pred. No. 4.4e-212; No. of
 Matches 528; Conservative 1; MisMatches 1; Indels 0; Gaps 0;

QY 1 MSFRSIALSGLVCTGLANVISKRATLDSMSLNBEATVARTAILNNIGAWGAWSGADSGI 60
 1 MSFRSIALSGLVCTGLANVISKRATLDSMSLNBEATVARTAILNNIGAWGAWSGADSGI 60

Db 61 WVASPTNDPYFTWTRDGLVLTLDLFRNGDTSLISTIENYISAQIVOGISINPSG 120
 61 WVASPTNDPYFTWTRDGLVLTLDLFRNGDTSLISTIENYISAQIVOGISINPSG 120

QY 121 DLSSGAGLGPKFKNDEATYGSGWGRPDRGPAKRALATAMIGFGQMLLDNGYTSTATDW 180
 121 DLSSGAGLGPKFKNDEATYGSGWGRPDRGPAKRALATAMIGFGQMLLDNGYTSTATDW 180

QY 181 PLVRNDLSVVAQYMNQTYGDLWEENGSSFTIAVQHRAVEGSAFATAVGSSCSWCDSQ 240
 181 PLVRNDLSVVAQYMNQTYGDLWEENGSSFTIAVQHRAVEGSAFATAVGSSCSWCDSQ 240

Db 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300
 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

SQ Sequence 640 AA;

QY 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Db 301 NHKEVUDSFRSIYTLNDGLSDESEAVALGARYPEDTYINGNPWFCLTAAEQLDALYQMD 360

QY 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

Db 361 KQGSLEVTDVSLDFKKALYSDAATGTYSSSSSTTSSIVDAVKTFADGFVISVETHAASNG 420

SQ Sequence 640 AA;

QY 241 APEILCYLOSFWTGSFLIANFDSSGKDANTLIGSIHPPDEACDSDFQPCSPRALA 300

Qy 421 SMSEQTDKSDGEQLSARDLTLWSYALITANRNSVPAWGETSASSVPGTCAATSAIG 480
 Db 421 SMSEQYQKSKDGEQLSARDLTLWSYALITANRNSVPAWGETSASSVPGTCAATSAIG 480
 Qy 481 TYSVTWSPSIVATGGTTATPGSGSVTSTSCTSKTSTTRS 530
 Db 481 TYSVTWSPSIVATGGTTATPGSGSVTSTSCTSKTSTTRS 530

RESULT 9

ID AAP40212 standard; protein: 639 AA.
 XX
 AC AAP40212;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-JAN-1992 (first entry)

Sequence encoded by A.awamori glucoamylase genomic region.

DE Starch hydrolysis; glucose.

KW Aspergillus awamori.

OS Aspergillus awamori.

PN WO8402921-A.
 XX
 PD 02-AUG-1994.
 XX
 PP 26-JAN-1984; 84WO-US000122.
 XX
 PR 28-JAN-1983; 83US-00461920.
 PR 20-DEC-1983; 83US-00563941.
 PR 27-APR-1987; 87US-00047552.

PA (CETU) CIRUS CORP.
 PA (CETU) CIRUS CORP.
 PI Nurnberg JH, Flatgaard JE, Innis MA, Gelfand DH, Meade JH;
 XX
 DR WPI; 1984-201413/32.

XX DNA sequence coding for fungal glucoamylase protein - for expression in yeast etc. for prodn. of the enzyme.

XX Example; Table 1, Page 21-25; 66pp; English.

The inventors claim a modified DNA sequence coding for fungal glucoamylase protein or its single or multiple base substitutions derived deletions, insertions or inversions is new (see AN40165). It is derived from natural, synthetic or semisynthetic sources and is capable, when correctly combined with a cleaved expression vector, of expressing a non-native protein having glucoamylase activity on transformation of a host organism by the vector. (Updated on 25-MAR-2003 to correct PI field.)

SQ Sequence 639 AA:

Query Match 96.8%; Score 2683.5; DB 1; Length 639;
 Best Local Similarity 98.1%; Preq. No. 2.3e-207; Mismatches 520; Conservative 1; Indels 1; Gaps 1; Matches 1;

Qy 1 MSFRSLLLASLSCVLTGLANVSKRATLDSWISNEATVARTAILNNAGDAWGNGADSGI 60
 Db 1 MSFRSLLLASLSCVLTGLANVSKRATLDSWISNEATVARTAILNNAGDAWGNGADSGI 60

Qy 61 TVASPSTDNPYPFTWRDSLQVLUKLVLDRNGDTSLSLTIENYISAQIVQGSNPSG 120
 Db 61 TVASPSTDNPYPFTWRDSLQVLUKLVLDRNGDTSLSLTIENYISAQIVQGSNPSG 120

Qy 121 DLSSGAGLGERKFKNVDETAYTGSGWGRQRDGPALARATAMGFGQWILDNGTSTATDIV 180
 Db 121 DLSSG-GIGEPKFNVDETAYTGSGWGRQRDGPALARATAMGFGQWILDNGTSTATDIV 179

RESULT 10

ID AAP81876
 ID AAP81876 standard; protein: 630 AA.
 XX
 AC AAP81876;
 XX
 PR 24-OCT-2003 (revised)
 PR 25-MAR-2003 (revised)
 DT 15-MAR-1992 (first entry)

DB Sequence of amyloglucosidase.

XX Enzyme; brewing; bread-making; dextrin.

OS Aspergillus niger; NCI 22343.
 XX
 PN BP260160-A.
 XX
 PD 16-MAR-1988.
 XX
 PP 10-JUN-1987; 87EP-00401300.
 XX
 PR 10-JUN-1986; 86FR-00008387.
 PR 13-APR-1987; 87FR-00005207.
 PR 13-APR-1987; 87FR-00005208.

PA (TRGE) TRANSGENE SA.
 PA Labat N, Loison G, Lemoine Y;
 PR WPI; 1988-072593/11.
 PR DR N-PSDB; AN82019.

XX New DNA block for expressing amyloglucosidase in yeast - contg. gene plus transcription and export sequences, and transformed cells useful in brewing and bread making.

XX Example; Fig 2; 38pp; French.

CC ECORI-Sal I fragments of Aspergillus niger NCI 22343 were cloned in PCR22 and two clones contg. portions of the gene isolated using a pool of three probes-TG82, TG283, TG84-(AN82014-6) designed on the basis of already published SOs. The clones were designated pTG130 and 1831. A cDNA bank of A. niger NCI 22343 was screened for amyloglucosidase using probe TG43 (AN82017) which corresponded to AAs 163-172 of the mature protein (see AN82019). Oligo TG37 (AN82018) was used to confirm the identity of the clones detected. (Updated on 25-MAR-2003 to correct PR

Qy 181 PLVRNDISYQYQWMNTGYDLEWEYNGSSFTIAVORHALVEGSAFATAVGSSCSMDSQ 240
 Db 180 PLVRNDISYQYQWMNTGYDLEWEYNGSSFTIAVORHALVEGSAFATAVGSSCSMDSQ 239

Qy 241 APICLVLQSQWTGSPFLANFDSSRSRKDANTLGSIHTDPPEACDDSTFOPCSPPALA 300
 Db 240 APICLVLQSQWTGSPFLANFDSSRSRKDANTLGSIHTDPPEACDDSTFOPCSPPALA 299

Db 300 NHKEVUDFSRISIYTTLANGLSDSEAVAVGRYEDTYGNPFLCTLAASQYDALYQWD 359

Qy 361 KQGSLVTVTDLSDFFKALYSPAATGSSSSSTYISIVDAVKTADGFVSVETHAHSNG 420
 Db 360 KQGSLVTVTDLSDFFKALYSPAATGSSSSSTYISIVDAVKTADGFVSVETHAHSNG 419

Qy 421 SMSEQTDKSDGEQLSARDLTLWSYALITANRNSVPAWGETSASSVPGTCAATSAIG 480
 Db 420 SMSEQTDKSDGEQLSARDLTLWSYALITANRNSVPAWGETSASSVPGTCAATSAIG 479

Qy 481 TYSVTWSPSIVATGGTTATPGSGSVTSTSCTSKTSTTRS 530
 Db 480 TYSVTWSPSIVATGGTTATPGSGSVTSTSCTSKTSTTRS 529

CC	Query Match	95.9%; Score 2658; DB 1; Length 630;	DR	WPI: 2000-514725/46.
XX	Best Local Similarity	97.2%; Pred. No. 2.6e-205;	XX	Fungal glucoamylase for selective production of glucose rather than alpha-D-glucan glucohydrolase;
CC	Matches	515; Conservative 2; Mismatches 3; Indels 10; Gaps 1;	PT	-1,6 linked disaccharide isomaltose, has mutation pair Asn20Cys coupled with Alaz2Cys forming disulfide bond between the two stabilizing members.
XX	OQ	1 MSFRSLLAISGLVCTGLANVSKRATLDSMSNEATAVTAIINNIGADGAWSGADSGI 60	PT	the nonreducing ends of maltooligosaccharides, attacking alpha-(1,4)-,
DB	1 MSFRSLLAISGLVCTGLANVSKRATLDSMSNEATAVTAIINNIGADGAWSGADSGI 60	CC	and alpha-(1,6)-glucosidic bonds.	
QY	61 WVASSTNDNFYFYTWRDGLVLTIVLWLRNGTSLSLTIENISAOIIVQGSNPG 120	CC	The present invention relates to mutant glucoamylases (see ABIL178-15184), which have increased thermostability, increased pH optimum and reduced isomaltose formation.	
DB	61 WVASSTNDNFYFYTWRDGLVLTIVLWLRNGTSLSLTIENISAOIIVQGSNPG 120	CC	The mutant proteins are useful for the selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose	
QY	121 DLSSAGLGEPKFNDETAVTGSWQRQD-----GPQONLNDGTSITADIW 170	CC		
DB	121 DLSSAGLGEPKFNDETAVTGSWQRQD-----GPQONLNDGTSITADIW 170	XX		
QY	181 PLVRUDLSSLYAQWYQWOTGYDWEEENGSSFTIAVORHALVEGSIPTAVGSSCWQSDO 240	SQ	Sequence 630 AA;	
DB	171 PLVRUDLSSLYAQWYQWOTGYDWEEENGSSFTIAVORHALVEGSIPTAVGSSCWQSDO 230	Query Match	94.8%; Score 2628; DB 3; Length 616;	
OQ	241 APEICYLQSFWTGSPFLANFDSSSGKDANTLSSIHFTDEPEAMDDSTFOPCSRALA 300	Best Local Similarity	99.6%; Pred. No. 6.5e-203;	
DB	231 APEICYLQSFWTGSPFLANFDSSSGKDANTLSSIHFTDEPEAMDDSTFOPCSRALA 290	Matches	504; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
QY	301 NHKEYVDSFRSYIYTANDGSDSEAYAVGRPEDTYNGNPFCLTAAALPOLYDLYQWD 360	OQ	25 ATLDSSLSNEATAVTAIINNIGADGAWSGADSGI 84	
DB	351 KQGSLEVTDVSLDFKALYSDAATGTYSSSTYSSIVDAVKTFRDGFSIVETHASNG 420	DB	1 ATLDSSLSNEATAVTAIINNIGADGAWSGADSGI 84	
QY	291 NHKEYVDSFRSYIYTANDGSDSEAYAVGRPEDTYNGNPFCLTAAALPOLYDLYQWD 350	QY	85 KTLVDFPFGNTSLISTENISAOIIVQGSNPGSDLSSGGAGLGEPKFNDETAVTGSW 144	
DB	361 KQGSLEVTDVSLDFKALYSDAATGTYSSSTYSSIVDAVKTFRDGFSIVETHASNG 420	DB	61 KTLVDFPFGNTSLISTENISAOIIVQGSNPGSDLSSGGAGLGEPKFNDETAVTGSW 120	
QY	421 SMSEQYDKSGSGBQLSARDLTVMSYALLTANRRNSVVPASWGETSASSVPGTCAIAG 480	QY	145 GRPORDGPALRATAMIGFGQWLLNDGYSTADTIVPLVPLVRNDLSVYAQWYQDLYQWD 60	
DB	411 SMSEQYDKSGSGBQLSARDLTVMSYALLTANRRNSVVPASWGETSASSVPGTCAIAG 470	DB	121 GRPORDGPALRATAMIGFGQWLLNDGYSTADTIVPLVPLVRNDLSVYAQWYQDLYQWD 180	
QY	481 TYSSVTVSNSPIVATGTTTATPGSGSVTSTKTTASKTSTTRS 530	QY	205 WNGSSEFTIYOHRALEVEGSAFATVGSSCWQSOAPEICYLQSFWTGSPFLANFDSS 264	
DB	471 TYSSTVTVSNSPIVATGTTTATPGSGSVTSTKTTASKTSTTRS 520	DB	181 VNGSSPFTIYOHRALEVEGSAFATVGSSCWQSDQSAPEICYLQSFWTGSPFLANFDSS 240	
RESULT 11	AAB15176 standard; protein; 616 AA.	QY	265 FSGKDANTLSSIHFTDEPEAMDDSTFOPCSRALA 300	
ID	AAB15176	DB	241 RSGKDANTLSSIHFTDEPEAMDDSTFOPCSRALA 300	
XX	AAB15176;	QY	325 VAGRYPEDTYNGNPFCLTAAALPOLYDLYQWDKQGSLEVTDVSLDFKALYSDAAT 360	
DT	11-DEC-2000 (first entry)	DB	301 VAGRYPEDTYNGNPFCLTAAALPOLYDLYQWDKQGSLEVTDVSLDFKALYSDAAT 360	
XX	Aspergillus awamori glucoamylase.	QY	385 GTYSSSSSTYSSIVDAVKTFRDGFSIVETHASNGSMSQYDKDGEQFASRDITWSA 444	
DE	Aspergillus awamori glucoamylase.	DB	361 GTYSSSSSTYSSIVDAVKTFRDGFSIVETHASNGSMSQYDKDGEQFASRDITWSA 420	
XX	KW Glucoamylase; enzyme; carbohydrate; glucose; 1,4-alpha-D-glucan glucohydrolase.	QY	445 ALLTANRRNSVVPASWGETSASSVPGTCAIAGTYSVVTWSPIVATGGTTAT 504	
OS	Aspergillus awamori.	DB	421 ALLTANRRNSVVPASWGETSASSVPGTCAIAGTYSVVTWSPIVATGGTTAT 480	
XX	WO200043504-A1.	QY	505 PTGSGSVTSTKTTASKTSTTRS 530	
PN		DB	481 PTGSGSVTSTKTTASKTSTTRS 506	
XX	22-JAN-1999; 99US-00236063.	RESULT 12		
XX	27-JUL-2000.	AAW55979		
XX	10-JAN-2000; 20000W0-US00532.	ID	AAW55979 standard; protein; 616 AA.	
XX		XX		
PR	(IOWA) UNIV IOWA STATE RES FOUND INC.	AC	AAW55979;	
PA	Allen MJ, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R;	XX		
PI	Ford C;	DT	27-JUL-1998 (first entry)	

KW genetic engineering.

XX OS Synthetic.

OS Aspergillus awamori.

XX PN WO9813639-A1.

XX PD 29-JAN-1998.

XX PR 24-JUL-1997; 97WO-US012983.

XX PR 24-JUL-1996; 96US-0022378P.

XX PA (IOWA) UNIV IOWA STATE RES FOUND INC.

XX PI Allen M., Fang T., Li Y., Liu H., Chen H., Coutinho P., Honzatko R.; Ford C.; DR WPI; 1998-120764/11.

XX PT Genetically engineered fungal glucoamylase - useful in, e.g. food industry for production of high fructose corn sweeteners.

XX PS Claim 10; Page: 97pp; English.

XX CC The present sequence represents a specifically claimed mutant glucoamylase from *Aspergillus awamori* (1,4-alpha-D-glucan glucohydrolase). The present invention describes fungal glucoamylases (FG) comprising: a mutation pair Asn20Cys coupled with Ala27Cys forming a disulphide bond between the 2 members of the pair; and a 311-314loop or Ser411Ala mutation. FG can be used in industry for the production of high fructose corn sweeteners, while the glucose produced by glucoamylase can be crystallised or used in fermentation to produce organic products, e.g. citric acid, ascorbic acid, lysine, glutamic acid or ethanol for beverages and fuel. The mutations provide increased thermal stability, reduced isomaltose formation and increased pH optimum. N.B. The present sequence is not given in the specification but is derived from SEQ ID NO:1 as stated in the claim.

XX SQ Sequence 616 AA;

Query Match 94.7%; Score 2625; DB 2; Length 616;
Best Local Similarity 99.4%; Pred. No. 1.1e-202; Matches 503; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATLDLSLNSNEATVARTAILNNIGADGAWVGAGSDGTVVASPTNDPYFTWTRDSGLVL 84
Db 1 ATLDLSLNSNEATVARTAILNNIGADGAWVGAGSDGTVVASPTNDPYFTWTRDSGLVL 60

QY 85 KTLVLDFRNGTSLSTIENITISAQAVQOGNSPNSDLSSEASAGLGPKEWNTDEATVGSW 144
Db 61 KTLVLDFRNGTSLSTIENITISAQAVQOGNSPNSDLSSEASAGLGPKEWNTDEATVGSW 120

QY 145 GRPQRQGPALATAMGFGQMLNDGYTSTDIVPLVRDLSTVQAQYMQTGIDLWE 204
Db 121 GRPQRQGPALATAMGFGQMLNDGYTSTDIVPLVRDLSTVQAQYMQTGIDLWE 180

QY 205 VNGSSFTTIAVORHALVEGSAFATAVGSSCSWCDSQAPELCYLOGFWTSFILANFDSS 264
Db 181 VNGSSFTTIAVORHALVEGSAFATAVGSSCSWCDSQAPELCYLOGFWTSFILANFDSS 240

QY 265 RSGKDANTLGSISHTDPPEACADDSTPQCSPRALANKHEVDSFRSYIYLNDGLSDSEA 324
Db 241 RSGKDANTLGSISHTDPPEACADDSTPQCSPRALANKHEVDSFRSYIYLNDGLSDSEA 300

QY 325 WAVGRYPEDTYTGNPFLCTLAAPOLYDLYQMDKGSELEVDYSLDFPKALYDAAT 384
Db 301 WAVGRYPEDTYTGNPFLCTLAAPOLYDLYQMDKGSELEVDYSLDFPKALYDAAT 360

QY 385 GTYSSSSTSISIVDAVKTADGFVSIVETMASNSMSMSEQYDKSDBQLSARDJTWYA 444
Db 361 GTYSSSSTSISIVDAVKTADGFVSIVETMASNSMSMSEQYDKSDBQLSARDJTWYA 420

RESULT 13 AAB15180
ID AAB15180 standard; protein; 616 AA.
XX AC AAB15180;
XX DT 11-DEC-2000 (first entry)
XX DE Aspergillus awamori mutant glucoamylase S411A substitution.
XX Glucamylase; enzyme; carbohydrate; glucose;
KW 1,4-alpha-D-glucan glucohydrolase; mutein; mutation.
XX OS Aspergillus awamori.
OS Synthetic.

XX Key Location/Qualifiers
FH Misc-difference 411
PT /note= "Wild-type Ser substituted by Ala"
XX BN WO20043504-A1.
XX PD 27-JUL-2000.
XX PP 10-JAN-2000; 2000WO-US000532.
XX PR 22-JAN-1999; 99US-00236063.
XX PA (IOWA) UNIV IOWA STATE RES FOUND INC.
XX PI Allen MJ., Fang T., Li Y., Liu H., Chen H., Coutinho P., Honzatko R.;
PT Ford C.; DR WPI; 2000-514725/46.

XX PT Fungal glucoamylase for selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose, has mutation pair Asn20Cys coupled with Ala27Cys forming disulfide bond between the two stabilizing members.

XX PS Claim 10; Page: 160pp; English.

XX CC Glucoamylase (1,4-alpha-D-glucan glucohydrolase; E.C. 3.2.1.3) is a carbohydrate. This enzyme cleaves D-glucose from the non-reducing ends of maltooligosaccharides, attacking alpha-(1,4)-, and alpha-(1,6)-glucosidic bonds. The present invention relates to mutant glucoamylases, which have increased thermostability, increased pH optimum and reduced isomaltose formation. The mutant proteins are useful for the selective production of glucose rather than alpha-1,6 linked disaccharide isomaltose. The present sequence is one such mutant enzyme. Note: The present sequence is not shown in the specification but is derived from the *Aspergillus awamori* wild-type glucoamylase sequence given in pages 152-153 of the sequence listing (SEQ ID 1).

XX SQ Sequence 616 AA;

Query Match 94.7%; Score 2625; DB 3; Length 616;
Best Local Similarity 99.4%; Pred. No. 1.1e-202; Matches 503; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 25 ATLDLSLNSNEATVARTAILNNIGADGAWVGAGSDGTVVASPTNDPYFTWTRDSGLVL 84
Db 1 ATLDLSLNSNEATVARTAILNNIGADGAWVGAGSDGTVVASPTNDPYFTWTRDSGLVL 60

QV 85 KTLVLDLFRGDTSLISTENYISAQAIYQISNPGDLSGGAGCIGEPKENVDETAIYGGSW 144
 Db 61 KTLVLDLFRGDTSLISTENYISAQAIYQISNPGDLSGGAGCIGEPKENVDETAIYGGSW 120
 QY 145 GRPORDGPALRATAMIGFQWLIDNGYSTADIVWPLVRNDLSYVAQWNQTYDLSWE 204
 Db 121 GRPORDGPALRATAMIGFQWLIDNGYSTADIVWPLVRNDLSYVAQWNQTYDLSWE 180
 QY 205 VNGSSFTAVQHRLALVEGSAFATAVGSSCSWCDSQAPEILCYLQSFWTGSPFLANFDSS 264
 Db 181 VNGSSFTAVQHRLALVEGSAFATAVGSSCSWCDSQAPEILCYLQSFWTGSPFLANFDSS 240
 QY 265 RSGKDANTLIGSHTFDPBACCDSTFOCPSPRALANKEVUVDSFRSIYTNLGLSSEA 324
 Db 241 RSGKDANTLIGSHTFDPBACCDSTFOCPSPRALANKEVUVDSFRSIYTNLGLSSEA 300
 QY 325 VAVGYPEDTYYNGNPWFCLTAAEQLDQYDALKYQDQKGSLEVTDVSLDFKALYSDAAT 384
 Db 301 VAVGYPEDTYYNGNPWFCLTAAEQLDQYDALKYQDQKGSLEVTDVSLDFKALYSDAAT 360
 QY 385 GTVSSSSSYSTIVDAVKTFADGFSIVETHAASNMSSEQYDKSDGQSLARDLTWSYA 444
 Db 361 GTVSSSSSYSTIVDAVKTFADGFSIVETHAASNMSSEQYDKSDGQSLARDLTWSYA 420
 QY 445 ALLTANNRNRNSVVPASWGETSASSVPGTCATAAIGTSSVVTWSWPSIVATGTTTAT 504
 Db 421 ALLTANNRNRNSVVPASWGETSASSVPGTCATAAIGTSSVVTWSWPSIVATGTTTAT 480
 QY 505 PTSGSGSVTSTSKTTATASKTTTRS 530
 Db 481 PTSGSGSVTSTSKTTATASKTTTRS 506

RESULT 14

AAW55976 standard; protein; 616 AA.

XX AAW55976;
 XX DT 27-JUL-1998 (first entry)
 DE Aspergillus awamori glucoc Amylase mutant N20C, A27C.
 XX KW Aspergillus awamori; glucoc Amylase; Aspergillus sp.; mutant; fungal; food; genetic engineering.
 KW OS Synthetic.
 OS Aspergillus awamori.
 XX FH Key location/Qualifiers
 FF Disulfide-bond 20. .27
 XX PN W09803639-A1.
 XX PD 29-JAN-1998.
 XX PF 24-JUL-1997; 97WO-US012983.
 XX PR 24-JUL-1996; 96US-0022578P.
 PR 02-AUG-1996; 96US-0033077P.
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 PI Allen M, Fang T, Li Y, Liu H, Coutinho P, Honzatko R;
 PI Ford C;
 XX DR WPI; 1998-120764/11.

PT Genetically engineered fungal glucoc Amylase - useful in, e.g. food industry for production of high fructose corn sweeteners.

PS Claim 1, Page: 97pp; English.

Query Match 94.4%; Score 2615; DB 2; Length 616;
 Best local Similarity 99.2%; Pred. No. 7.3e-202; Mismatches 1; Indels 0; Gaps 0;
 Matches 502; Conservative 1; MisMatches 3; Indels 0; Gaps 0;

QY 25 ATUDSWLSHEATARVARTAILNNGADGAWMSGADGIVASASPSTDNPYFTWMDSCVL 84
 ID 1 ATUDSWLSHEATARVARTAILNNGADGAWMSGADGIVASASPSTDNPYFTWMDSCVL 60

Db 85 KTLVLDLFRGDTSLISTENYISAQAIYQISNPGDLSGGAGCIGEPKENVDETAIYGGSW 144
 Db 61 KTLVLDLFRGDTSLISTENYISAQAIYQISNPGDLSGGAGCIGEPKENVDETAIYGGSW 120
 QY 145 GRPORDGPALRATAMIGFQWLIDNGYSTADIVWPLVRNDLSYVAQWNQTYDLSWE 204
 Db 121 GRPORDGPALRATAMIGFQWLIDNGYSTADIVWPLVRNDLSYVAQWNQTYDLSWE 180
 QY 205 VNGSSFTAVQHRLALVEGSAFATAVGSSCSWCDSQAPEILCYLQSFWTGSPFLANFDSS 264
 Db 181 VNGSSFTAVQHRLALVEGSAFATAVGSSCSWCDSQAPEILCYLQSFWTGSPFLANFDSS 240
 QY 265 RSGKDANTLIGSHTFDPBACCDSTFOCPSPRALANKEVUVDSFRSIYTNLGLSSEA 324
 Db 241 RSGKDANTLIGSHTFDPBACCDSTFOCPSPRALANKEVUVDSFRSIYTNLGLSSEA 300
 QY 325 VAVGYPEDTYYNGNPWFCLTAAEQLDQYDALKYQDQKGSLEVTDVSLDFKALYSDAAT 384
 Db 301 VAVGYPEDTYYNGNPWFCLTAAEQLDQYDALKYQDQKGSLEVTDVSLDFKALYSDAAT 360
 QY 385 GTVSSSSSYSTIVDAVKTFADGFSIVETHAASNMSSEQYDKSDGQSLARDLTWSYA 444
 Db 361 GTVSSSSSYSTIVDAVKTFADGFSIVETHAASNMSSEQYDKSDGQSLARDLTWSYA 420
 QY 445 ALLTANNRNRNSVVPASWGETSASSVPGTCATAAIGTSSVVTWSWPSIVATGTTTAT 504
 Db 421 ALLTANNRNRNSVVPASWGETSASSVPGTCATAAIGTSSVVTWSWPSIVATGTTTAT 480
 QY 505 PTSGSGSVTSTSKTTATASKTTTRS 530
 Db 481 PTSGSGSVTSTSKTTATASKTTTRS 506

RESULT 15

AAB15178 standard; protein; 616 AA.

XX AC AAB15178;
 XX DT 11-DEC-2000 (first entry)
 XX DB Aspergillus awamori mutant glucoc Amylase N20C/A27C substitution.
 XX KW Glucoc Amylase; enzyme; carbohydrate; glucose;
 KW 1,4-alpha-D-glucan glucohydrolase; mutant; mutation.
 XX OS Aspergillus awamori.
 OS Synthetic.

Poss Note

XX	Key	Location/Qualifiers
FH	Disulfide-bond	20. .27
FT	Misc-difference	20 /note= "Wild-type Asn substituted by Cys"
FT	Misc-difference	27 /note= "Wild-type Ala substituted by Cys"
XX	PN	WO20043504-A1.
XX	PD	27-JUL-2000.
XX	PR	10-JAN-2000; 2000WO-US000532.
XX	PR	22-JAN-1999; 99US-00236063.
XX	PA	(IOWA) UNIV IOWA STATE RBS FOUND INC.
PI	Allen MJ, Fang T, Li Y, Liu H, Chen H, Coutinho P, Honzatko R;	
PI	Ford C;	
XX		
DR		
XX	PT	Fungal glucoamylase for selective production of glucose rather than alpha-1,6 linked diaccharide isomaltose, has mutation pair Asn20Cys coupled with Ala27Cys forming disulfide bond between the two stabilizing members.
PS	Claim 1; Page; 160pp; English.	
CC	Glucosidase (1, 4-alpha-D-glucan glucohydrolase; E.C. 3.2.1.3) is a carbohydrate. This enzyme cleaves D-glucose from the nonreducing ends of maltoligosaccharides, attacking alpha-(1,4)- and alpha-(1,6)-glucosidic bonds. The present invention relates to mutant glucoamylases, which have increased thermostability, increased pH optimum and reduced isomaltose formation. The mutant proteins are useful for the selective production of glucose rather than alpha-1,6 linked diaccharide isomaltose. The present sequence is one such mutant enzyme. Note: The present sequence is not shown in the specification but is derived from the Aspergillus awamori wild-type glucoamylase sequence given in pages 152-153 of the sequence listing (SEQ ID 1)	
SQ	Sequence 616 AA:	
94.4%; Score 2615; DB 3; Length 616;		
Query Match 99.2%; Pred. No. 7.3e-202; Matches 502; Conservative 1; Mismatches 3; Indels 0; Gaps 0;		
QY	25 ATLDLSLNEATVARTAILNIGADAWWSADSGITWASPTSTDNDYFWTWRDQLVL	84
Db	1 ATLDLSLNEATVARTAILNIGADCGWWSADSGIVASBSTDNDYFWTWRDQLVL	60
QY	85 KTLVDFRNGTSLSLTIENTSQAIVQGSNPGLSSAGLGPKFNEDETAYTGSW	144
Db	61 KTLVDFRNGTSLSLTIENTSQAIVQGSNPGLSSAGLGPKFNEDETAYTGSW	120
QY	145 GRPQRDGPALEAMTGFGQNLNDGTYSTADIVPLVRNDLSYYAQYNNQGTGDWEE	204
Db	121 GRPQRDGPALEAMTGFGQNLNDGTYSTADIVPLVRNDLSYYAQYNNQGTGDWEE	180
QY	205 VNGSSFTIATVORHALVEGSAFATAVGSSCCWCDSDAPEIICYLQSFWTSSFTLANFDSS	264
Db	181 VNGSSFTIATVORHALVEGSAFATAVGSSCCWCDSDAPEIICYLQSFWTSSFTLANFDSS	240
QY	265 RSGKDANTLGSIHTDPDEAACDDSFQPCSPRALNHKEYVDSRSIYIYNGLSEA	324
Db	241 RSGKDANTLGSIHTDPDEAACDDSFQPCSPRALNHKEYVDSRSIYIYNGLSEA	300
QY	325 VAVGRYPDTTYNGNPMPLCTIAAEQLYDLYQWDKQGSIETVDVSLDFFRALYSDAAT	384
Db	301 VAVGRYPDTTYNGNPMPLCTIAAEQLYDLYQWDKQGSIETVDVSLDFFRALYSDAAT	360
QY	385 GTYSSSSSTYISIVDAVKTFAIDGFVSVIETHASNSMSBQYDKSGEOLSLARDLWYA	444

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post dated Page 1
a. P. V. C. M.

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: June 17, 2004, 17:47:36 ; Search time 50 Seconds
(without alignments)

3015.110 Million cell updates/sec
US-10-038-723-2

Perfect score: 2771
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues
Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgm2_6/prodata/1/pubpaas/US07_PUBCOMB.pep: *
2: /cgm2_6/prodata/1/pubpaas/PCT NEW PUB.pep: *
3: /cgm2_6/prodata/1/pubpaas/US06_PUBCOMB.pep: *
4: /cgm2_6/prodata/1/pubpaas/US06_PUBCOMB.pep: *
5: /cgm2_6/prodata/1/pubpaas/US07 NEW PUB.pep: *
6: /cgm2_6/prodata/1/pubpaas/PCTUS_PUBCOMB.pep: *
7: /cgm2_6/prodata/1/pubpaas/US08 NEW PUB.pep: *
8: /cgm2_6/prodata/1/pubpaas/US08_PUBCOMB.pep: *
9: /cgm2_6/prodata/1/pubpaas/US09_PUBCOMB.pep: *
10: /cgm2_6/prodata/1/pubpaas/US09_PUBCOMB.pep: *
11: /cgm2_6/prodata/1/pubpaas/US09C_PUBCOMB.pep: *
12: /cgm2_6/prodata/1/pubpaas/US09_NEW PUB.pep: *
13: /cgm2_6/prodata/1/pubpaas/US10_PUBCOMB.pep: *
14: /cgm2_6/prodata/1/pubpaas/US10_PUBCOMB.pep: *
15: /cgm2_6/prodata/1/pubpaas/US10C_PUBCOMB.pep: *
16: /cgm2_6/prodata/1/pubpaas/US10C_PUBCOMB.pep: *
17: /cgm2_6/prodata/1/pubpaas/US60 NEW PUB.pep: *
18: /cgm2_6/prodata/1/pubpaas/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
US-09-908-395-2
Sequence 2, Application US/09908395
; Parent No. US20020164723A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Gin
; APPLICANT: Pedersen, Sven
; APPLICANT: Hendriksen, Sven
TITLE OF INVENTION: A Method of Producing Saccharide
FILE REFERENCE: 5318-200-US
CURRENT APPLICATION NUMBER: US/09/908,395
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US/09/198,672
PRIOR FILING DATE: PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 534
TYPE: PRT
ORGANISM: Aspergillus Niger
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(24)
US-09-908-395-2

Query Match 100.0%; Score 2771; DB 9; Length 534;
Best Local Similarity 100.0%; Pred. No. 2.7e-237;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFRSLALSGLVCTGLANVSKRATLSMSNEATVARTAIIINNIGDAGAWSGADSGI 60
DB 1 MSFRSLALSGLVCTGLANVSKRATLSMSNEATVARTAIIINNIGDAGAWSGADSGI 60

QY 61 WVASSTDNDPYFYWTRDSGLVLUKTLDFRRNGDTSLISTIENIYSAQIVQGSNPSG 120
DB 61 WVASSTDNDPYFYWTRDSGLVLUKTLDFRRNGDTSLISTIENIYSAQIVQGSNPSG 120

Sequence 13, Appl
Sequence 10, Appl
Sequence 16, Appl
Sequence 19, Appl
Sequence 30, Appl
Sequence 38, Appl
Sequence 26, Appl

Result No.	Score	Query Match Length	DB ID	Description
1	2771	100.0	534 9	US-09-908-395-2 Sequence 2, Appli Sequence 9, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 13, Appli Sequence 14, Appli Sequence 9, Appli Sequence 13, Appli Sequence 10, Appli Sequence 16, Appli Sequence 19, Appli Sequence 30, Appli Sequence 38, Appli Sequence 26, Appli

QY 121 DLSSGAGIGEPKENVDETYTGSWGRPQDGPA RATAMIGFQWLNGYSTADIVW 180
Db 121 DLSSGAGIGEPKENVDETYTGSWGRPQDGPA RATAMIGFQWLNGYSTADIVW 180
QY 181 PLVRNDLSVVAQWNQOTGDLWEVNGSSPFTAVQRALVEGSAFATAVGSSCWCSQ 240
Db 181 PLVRNDLSVVAQWNQOTGDLWEVNGSSPFTAVQRALVEGSAFATAVGSSCWCSQ 240
QY 241 APEILCYQSFWTGSPFLANPDSRSKGDA NTLGSIMTFDPEACDSTFOPCSPRALA 300
Db 241 APEILCYQSFWTGSPFLANPDSRSKGDA NTLGSIMTFDPEACDSTFOPCSPRALA 300
QY 301 NHKEVVDSPRSITYLNDGLSDSEAVAVGRYPEDTYNQNPWFCTLAQEQLDALYQWD 360
Db 301 NHKEVVDSPRSITYLNDGLSDSEAVAVGRYPEDTYNQNPWFCTLAQEQLDALYQWD 360
QY 361 KQSSL ETVDSLDFPKALYSDAATGTYSSS TSYSSIVDAVKTFADGVSVI VETHAASNG 420
Db 361 KQSSL ETVDSLDFPKALYSDAATGTYSSS TSYSSIVDAVKTFADGVSVI VETHAASNG 420
QY 421 SMSRQYDSDGEQSLARDLTWSYALLTANNRRNSVVPASWGETSASSVPGTCATSAIG 480
Db 421 SMSRQYDSDGEQSLARDLTWSYALLTANNRRNSVVPASWGETSASSVPGTCATSAIG 480
QY 481 TYSVTVTWSWPSIVATGGTTTAPTGGSVTSKTTASKSTTRSGMSL 534
Db 481 TYSVTVTWSWPSIVATGGTTTAPTGGSVTSKTTASKSTTRSGMSL 534
RESULT 2
US-09-821-616-9
; Sequence 9, Application US/09821616
; Publication No. US20030027290A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Nielsen, Ruby
; APPLICANT: Lehmbbeck, Jan
; TITLE OF INVENTION: Thermostable Glucoamylase
; FILE REFERENCE: 5279.200-US
; CURRENT APPLICATION NUMBER: US/09/821,616
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/199,290
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE: SIGNAL
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; US-09-821-616-9

QY 61 VVASPSTONPDYTFWTDGSLVLTLDLFRNGDTSLSIENYISQAIVCGISNSG 120
Db 61 VVASPSTONPDYTFWTDGSLVLTLDLFRNGDTSLSIENYISQAIVCGISNSG 120
QY 121 DLSSGAGIGEPKENVDETYTGSWGRPQDGPA RATAMIGFQWLNGYSTADIVW 180
Db 121 DLSSGAGIGEPKENVDETYTGSWGRPQDGPA RATAMIGFQWLNGYSTADIVW 180
QY 181 PLVRNDLSVVAQWNQOTGDLWEVNGSSPFTAVQRALVEGSAFATAVGSSCWCSQ 240
Db 181 PLVRNDLSVVAQWNQOTGDLWEVNGSSPFTAVQRALVEGSAFATAVGSSCWCSQ 240
QY 241 APEILCYQSFWTGSPFLANPDSRSKGDA NTLGSIMTFDPEACDSTFOPCSPRALA 300
Db 241 APEILCYQSFWTGSPFLANPDSRSKGDA NTLGSIMTFDPEACDSTFOPCSPRALA 300
QY 301 NHKEVVDSPRSITYLNDGLSDSEAVAVGRYPEDTYNQNPWFCTLAQEQLDALYQWD 360
Db 301 NHKEVVDSPRSITYLNDGLSDSEAVAVGRYPEDTYNQNPWFCTLAQEQLDALYQWD 360
QY 361 KQSSL ETVDSLDFPKALYSDAATGTYSSS TSYSSIVDAVKTFADGVSVI VETHAASNG 420
Db 361 KQSSL ETVDSLDFPKALYSDAATGTYSSS TSYSSIVDAVKTFADGVSVI VETHAASNG 420
QY 421 SMSRQYDSDGEQSLARDLTWSYALLTANNRRNSVVPASWGETSASSVPGTCATSAIG 480
Db 421 SMSRQYDSDGEQSLARDLTWSYALLTANNRRNSVVPASWGETSASSVPGTCATSAIG 480
QY 481 TYSVTVTWSWPSIVATGGTTTAPTGGSVTSKTTASKSTTRSGMSL 534
Db 481 TYSVTVTWSWPSIVATGGTTTAPTGGSVTSKTTASKSTTRSGMSL 534
RESULT 3
US-10-038-723-2
; Sequence 2, Application US/10038723
; Publication No. US20030032163A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Roenfeldt
; APPLICANT: Pedersen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Frandsen, Torben Peter
; TITLE OF INVENTION: Glucoamylase Variant
; FILE REFERENCE: 5636.200-US
; CURRENT APPLICATION NUMBER: US/10/038,723
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/351,814
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00937
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 01667
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,528
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/115,545
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; US-10-038-723-2

QY 1 MSFRSLLALSGLVCTGLANVSKRATDLSWLSNEATVARTA LNNIGADGAWVGADSGI 60
Db 1 MSFRSLLALSGLVCTGLANVSKRATDLSWLSNEATVARTA LNNIGADGAWVGADSGI 60

RESULT 6
US-10-038-723-13
; Sequence 13, Application US/10038723
; Publication No. US20030032163A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Roenfeldt
; APPLICANT: Svendsen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Frandsen, Torben Peter
; TITLE OF INVENTION: Glucoamylose Variants
; FILE REFERENCE: 5636.2/00-US
; CURRENT APPLICATION NUMBER: US/10/038,723
; CURRENT FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/351,814
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 00937
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PA 1998 01667
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,528
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/115,545
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-038-723-13

Query Match 99.0%; Score 2742; DB 14; Length 640;
Best Local Similarity 99.6%; Pred. No. 1.4e-234; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNATVARTAIIANNIGDAGAWVGADSGI 60
1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNATVARTAIIANNIGDAGAWVGADSGI 60
Db 61 WASPSTDNPDYFTWTDGLVLTIDLFRGDTSLISTENYISQAIVOGISNSG 120
Qy 61 WASPSTDNPDYFTWTDGLVLTIDLFRGDTSLISTENYISQAIVOGISNSG 120
Db 61 VVASPSTDNPDYFTWTDGLVLTIDLFRGDTSLISTENYISQAIVOGISNSG 120
Qy 121 DLSSGAGLGEPKENDETAITGSMGRPRDGPAKATMIGFCWMLDNGYSTADIW 180
121 DLSSGAGLGEPKENDETAITGSMGRPRDGPAKATMIGFCWMLDNGYSTADIW 180
Db 181 PLVRNDLSVVAQWNQGTDLWEEVNGSFFTIAVOHRAVESSAFATAVGSSCSWCDSQ 240
181 PLVRNDLSVVAQWNQGTDLWEEVNGSFFTIAVOHRAVESSAFATAVGSSCSWCDSQ 240
Qy 241 APEILCYQSFWSFGSPFLANFDSSRGKDANTLGSIMTFDPEACDSTFOPCSPRALA 300
241 APEILCYQSFWSFGSPFLANFDSSRGKDANTLGSIMTFDPEACDSTFOPCSPRALA 300
Db 301 NHKEVWDSFRSIYTINDGLSDSEAVAVGRYPEDTYNGNPWFCLTAAEQYDALYQWD 360
301 NHKEVWDSFRSIYTINDGLSDSEAVAVGRYPEDTYNGNPWFCLTAAEQYDALYQWD 360
Db 361 KQSSLLEVTDVSLDFPKALYSDAATGTSSSTSYSSITDAVKFADGVSVIETHAASNG 420
361 KQSSLLEVTDVSLDFPKALYSDAATGTSSSTSYSSITDAVKFADGVSVIETHAASNG 420
Qy 421 SMSQYQDSGEQSLARDLTWSAALITANNRNSVVPASWGETSASSVPGTCATSAIG 480
421 SMSQYQDSGEQSLARDLTWSAALITANNRNSVVPASWGETSASSVPGTCATSAIG 480
Db 481 TYSVTWSPSVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
481 TYSVTWSPSVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534
Db 481 TYSVTWSPSVATGGTTATPTGGSVTSKTTASKSTTRSGMSL 534

RESULT 7
US-10-421-586-14
; Sequence 14, Application US/10421586
; Publication No. US20040002142A1
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Ronfeldt
; APPLICANT: Svendsen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; APPLICANT: Frandsen, Torben Peter
; TITLE OF INVENTION: Glucoamylose Variants
; FILE REFERENCE: 5957.2/0-US
; CURRENT APPLICATION NUMBER: US/10/421,586
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 640
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-421-586-14

Query Match 99.0%; Score 2742; DB 15; Length 640;
Best Local Similarity 99.6%; Pred. No. 1.4e-234; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNATVARTAIIANNIGDAGAWVGADSGI 60
1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNATVARTAIIANNIGDAGAWVGADSGI 60
Db 1 MSFRSLALSGLVCTGLANVSKRATLDSWLSNATVARTAIIANNIGDAGAWVGADSGI 60

Qy 61 WASPSTDNPDYFTWTDGLVLTIDLFRGDTSLISTENYISQAIVOGISNSG 120
61 VVASPSTDNPDYFTWTDGLVLTIDLFRGDTSLISTENYISQAIVOGISNSG 120
Db 121 DLSSGAGLGEPKENDETAITGSMGRPRDGPAKATMIGFCWMLDNGYSTADIW 180
121 DLSSGAGLGEPKENDETAITGSMGRPRDGPAKATMIGFCWMLDNGYSTADIW 180
Qy 181 PLVRNDLSVVAQWNQGTDLWEEVNGSFFTIAVOHRAVESSAFATAVGSSCSWCDSQ 240
181 PLVRNDLSVVAQWNQGTDLWEEVNGSFFTIAVOHRAVESSAFATAVGSSCSWCDSQ 240
Db 241 APEILCYQSFWSFGSPFLANFDSSRGKDANTLGSIMTFDPEACDSTFOPCSPRALA 300
241 APEILCYQSFWSFGSPFLANFDSSRGKDANTLGSIMTFDPEACDSTFOPCSPRALA 300
Db 301 NHKEVWDSFRSIYTINDGLSDSEAVAVGRYPEDTYNGNPWFCLTAAEQYDALYQWD 360
301 NHKEVWDSFRSIYTINDGLSDSEAVAVGRYPEDTYNGNPWFCLTAAEQYDALYQWD 360

RESULT 8
US-10-418-836-9
; Sequence 9, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaining
; TITLE OF INVENTION: Production of Functional Antibodies in
; TITLE OF INVENTION: Filamentous Fungi
; FILE REFERENCE: GC741-2
; CURRENT APPLICATION NUMBER: US/10/418,836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373, 889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411,540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452,134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411,537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 743
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: fusion protein
; OTHER INFORMATION: fusion protein
; US-10-418-836-9

Query Match 98.7%; Score 2735; DB 15; Length 743;
Best Local Similarity 99.6%; Pred. No. 7.2e-234;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 1 MSFRSLALSLGIVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
Db 1 MSFRSLALSLGIVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60

Query 61 VVASPSTDNPYFYWTWDRSGLVLKVLVLDFRNGDTSLLSTIENYISAQAVQGISNPSG 120
Db 61 VVASPSTDNPYFYWTWDRSGLVLKVLVLDFRNGDTSLLSTIENYISAQAVQGISNPSG 120

Query 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMIGFGQWLIDNGYSTATIDW 180
Db 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMIGFGQWLIDNGYSTATIDW 180

Query 181 PLVRNDLSYVQYWNQTYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240
Db 181 PLVRNDLSYVQYWNQTYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240

Query 241 APEILCYLQSFWTGSPFLANFDSSKGKDANTLGSIHTEPPEACDDSTFOPCSPRALA 300
Db 241 APEILCYLQSFWTGSPFLANFDSSKGKDANTLGSIHTEPPEACDDSTFOPCSPRALA 300

Query 301 NHKEVUDSFRSYITLNDGLSDEAVAVGRYPEDTYINGNPWFCLTAAEQLDYQWD 360
Db 301 NHKEVUDSFRSYITLNDGLSDEAVAVGRYPEDTYINGNPWFCLTAAEQLDYQWD 360

RESULT 9
US-10-418-836-13
; Sequence 13, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaining
; TITLE OF INVENTION: Production of Functional Antibodies in
; TITLE OF INVENTION: Filamentous Fungi
; FILE REFERENCE: GC741-2
; CURRENT APPLICATION NUMBER: US/10/418, 836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373, 889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411, 540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452, 134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411, 537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 763
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE: fusion protein
; OTHER INFORMATION: fusion protein
; US-10-418-836-13

Query Match 98.7%; Score 2735; DB 15; Length 763;
Best Local Similarity 99.6%; Pred. No. 7.5e-234;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query 1 MSFRSLALSLGIVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60
Db 1 MSFRSLALSLGIVCTGLANVSKRATLDSWLSNEATVARTAILNNIGADGAWVGADSGI 60

Query 61 VVASPSTDNPYFYWTWDRSGLVLKVLVLDFRNGDTSLLSTIENYISAQAVQGISNPSG 120
Db 61 VVASPSTDNPYFYWTWDRSGLVLKVLVLDFRNGDTSLLSTIENYISAQAVQGISNPSG 120

Query 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMIGFGQWLIDNGYSTATIDW 180
Db 121 DLSSGAGLGERKFNVDTAYTGSGWGRQDGPALRATAMIGFGQWLIDNGYSTATIDW 180

Query 181 PLVRNDLSYVQYWNQTYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240
Db 181 PLVRNDLSYVQYWNQTYDILWEENGSSFTIAVORHALVEGSAFATAVGSSCWDSQ 240

Query 241 APEILCYLQSFWTGSPFLANFDSSKGKDANTLGSIHTEPPEACDDSTFOPCSPRALA 300
Db 241 APEILCYLQSFWTGSPFLANFDSSKGKDANTLGSIHTEPPEACDDSTFOPCSPRALA 300

Query 301 NHKEVUDSFRSYITLNDGLSDEAVAVGRYPEDTYINGNPWFCLTAAEQLDYQWD 360
Db 301 NHKEVUDSFRSYITLNDGLSDEAVAVGRYPEDTYINGNPWFCLTAAEQLDYQWD 360

```

RESULT 10
US-10-418-836-10
; Sequence 10, Application US/10418836
; Publication No. US20040018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Huaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; TITLE OF INVENTION: Filamentous Fungi
; CURRENT APPLICATION NUMBER: US/10/418,836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373,889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411,540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452,134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411,537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
; US-10-418-836-10

Query Match          98.7%; Score 2735; DB 15; Length 979;
Best Local Similarity 99.6%; Pred. No. 1.1e-233; Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match          98.7%; Score 2735; DB 15; Length 979;
Best Local Similarity 99.6%; Pred. No. 1.1e-233; Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Matches 527; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MSFRSLLAISGLVCGTGLANVISKRATLDSWLSNEATVARTAILNIGADGAWGAGDSGI 60
Db      1 MSFRSLLAISGLVCGTGLANVISKRATLDSWLSNEATVARTAILNIGADGAWGAGDSGI 60
Qy      1 MSFRSLLAISGLVCGTGLANVISKRATLDSWLSNEATVARTAILNIGADGAWGAGDSGI 60
Db      1 MSFRSLLAISGLVCGTGLANVISKRATLDSWLSNEATVARTAILNIGADGAWGAGDSGI 60
Qy      61 VVASPSTDNPDYFWTRDGLVLTKLVLDFRNGTSLSITIENYISAQIVQGSNPG 120
Db      61 VVASPSTDNPDYFWTRDGLVLTKLVLDFRNGTSLSITIENYISAQIVQGSNPG 120
Qy      61 VVASPSTDNPDYFWTRDGLVLTKLVLDFRNGTSLSITIENYISAQIVQGSNPG 120
Db      61 VVASPSTDNPDYFWTRDGLVLTKLVLDFRNGTSLSITIENYISAQIVQGSNPG 120
Qy      121 DLSSGAGLGEPKFNDETAYGWSGRPDRGPALRATAMIGFGQWLLONGYSTATDIVW 180
Db      121 DLSSGAGLGEPKFNDETAYGWSGRPDRGPALRATAMIGFGQWLLONGYSTATDIVW 180
Qy      121 DLSSGAGLGEPKFNDETAYGWSGRPDRGPALRATAMIGFGQWLLONGYSTATDIVW 180
Db      121 DLSSGAGLGEPKFNDETAYGWSGRPDRGPALRATAMIGFGQWLLONGYSTATDIVW 180
Qy      181 PLVRNDLSVVAQWMQNTGYDLWEENGSSFTAVQHRAVEGSAPATAVGSSCCWCDSQ 240
Db      181 PLVRNDLSVVAQWMQNTGYDLWEENGSSFTAVQHRAVEGSAPATAVGSSCCWCDSQ 240
Qy      241 APEIICYLQSFWTGCSFILANFDSSRGKONTLGSIHFPDEACDSTFOPCSPRALA 300
Db      241 APEIICYLQSFWTGCSFILANFDSSRGKONTLGSIHFPDEACDSTFOPCSPRALA 300
Qy      241 APEIICYLQSFWTGCSFILANFDSSRGKONTLGSIHFPDEACDSTFOPCSPRALA 300
Db      241 APEIICYLQSFWTGCSFILANFDSSRGKONTLGSIHFPDEACDSTFOPCSPRALA 300
Qy      301 NHKEVVDSSRSIYTUNDGLSDSEAVAVGRYPEDTYNGNPWFLCTIAARQQLDQYOWD 360
Db      301 NHKEVVDSSRSIYTUNDGLSDSEAVAVGRYPEDTYNGNPWFLCTIAARQQLDQYOWD 360
Qy      301 NHKEVVDSSRSIYTUNDGLSDSEAVAVGRYPEDTYNGNPWFLCTIAARQQLDQYOWD 360
Db      361 KQGSLBEVTDVSLDFKALYSDAATGYSSSSSTSSIVDAVKTPADGFISIVETHASNG 420
Qy      421 SMSEQYDKSDGEQISARDLWTAULTTANRNRNSVPASWGETSASSVPGTCATSAIG 480
Db      421 SMSEQYDKSDGEQISARDLWTAULTTANRNRNSVPASWGETSASSVPGTCATSAIG 480
Qy      481 TSSVTVTSPSIVATGGTTATPGSCSVTSTSKTATASKTTTR 529
Db      481 TSSVTVTSPSIVATGGTTATPGSCSVTSTSKTATASKTTTR 529
Qy      481 TSSVTVTSPSIVATGGTTATPGSCSVTSTSKTATASKTTTR 529
Db      481 TSSVTVTSPSIVATGGTTATPGSCSVTSTSKTATASKTTTR 529

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RESULT 12
 US-10-418-836-19
 ; Sequence 19, Application US/10418836
 ; Publication No. US20040018573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Power, Scott D.
 ; APPLICANT: Wang, Huaming
 ; APPLICANT: Ward, Michael
 ; TITLE OF INVENTION: Production of Functional Antibodies in
 ; Filamentous Fungi
 ; FILE REFERENCE: GC741-2
 ; CURRENT APPLICATION NUMBER: US/10/418, 836
 ; CURRENT FILING DATE: 2003-04-17
 ; PRIOR APPLICATION NUMBER: US 60/373, 889
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/411, 540
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/452, 134
 ; PRIOR FILING DATE: 2003-03-04
 ; PRIOR APPLICATION NUMBER: US 60/411, 537
 ; PRIOR FILING DATE: 2002-09-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatSEQ for Windows Version 4.0
 ; SEQ ID NO: 19
 ; LENGTH: 738
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein
 ; US-10-418-836-19

Query Match 98.2%; Score 2720.5; DB 15; Length 738;
 Best Local Similarity 98.5%; Pred. No. 4.0e-332; Matches 527; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 MSFRSIALSLSVCTGLANVISKRATIDSWISNEATVARTAILNNIGADGAWNSGADSGI 60
 Db 1 MSFRSIALSLSVCTGLANVISKRATIDSWISNEATVARTAILNNIGADGAWNSGADSGI 60

Qy 61 VVASPSTDNPYFYTWRDSDSVLKTVLVDLRNGDTSLSITENYISAQIVQGSNPSG 120
 Db 61 VVASPSTDNPYFYTWRDSDVLVKTLVDLFRNGDTSLSITENYISAQIVQGSNPSG 120

Qy 181 PLVRNDLSYYAQWQYNGTGYDILWEENGSSFTIAVQRALVEGSAFATAVGSSCWDSQ 240
 Db 121 DLSSGAGLGKEKFNDETAVGWSGRPRQDGPAKATAMIGFGQWLDNGYSTATDVW 180
 Db 121 DLSSGAGLGKEKFNDETAVGWSGRPRQDGPAKATAMIGFGQWLDNGYSTATDVW 180

Qy 181 PLVRNDLSYYAQWQYNGTGYDILWEENGSSFTIAVQRALVEGSAFATAVGSSCWDSQ 240
 Db 181 PLVRNDLSYYAQWQYNGTGYDILWEENGSSFTIAVQRALVEGSAFATAVGSSCWDSQ 240

Qy 241 APEILCYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTDPPEACCDSTFQPCSPRALA 300
 Db 241 APEILCYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTDPPEACCDSTFQPCSPRALA 300

Qy 301 NHKEVUDSFESIYTUNDGLSDSEAVAVGRYPEDTYINGNPWFCLTAAQOLYQWD 360
 Db 301 NHKEVUDSFESIYTUNDGLSDSEAVAVGRYPEDTYINGNPWFCLTAAQOLYQWD 360

Qy 361 KQGSLEVTDSLDFKALYSATGTYSSTSSTYSSIVDAVKTADGFVSIVETHAASNG 420
 Db 361 KQGSLEVTDSLDFKALYSATGTYSSTSSTYSSIVDAVKTADGFVSIVETHAASNG 420

RESULT 13
 US-10-418-836-30
 ; Sequence 30, Application US/10418836
 ; Publication No. US20040018573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Power, Scott D.
 ; APPLICANT: Wang, Huaming
 ; APPLICANT: Ward, Michael
 ; TITLE OF INVENTION: Production of Functional Antibodies in
 ; Filamentous Fungi
 ; FILE REFERENCE: GC741-2
 ; CURRENT APPLICATION NUMBER: US/10/418, 836
 ; CURRENT FILING DATE: 2003-04-17
 ; PRIOR APPLICATION NUMBER: US 60/373, 889
 ; PRIOR FILING DATE: 2002-04-18
 ; PRIOR APPLICATION NUMBER: US 60/411, 540
 ; PRIOR FILING DATE: 2002-09-18
 ; PRIOR APPLICATION NUMBER: US 60/452, 134
 ; PRIOR FILING DATE: 2003-03-04
 ; PRIOR APPLICATION NUMBER: US 60/411, 537
 ; PRIOR FILING DATE: 2002-09-18
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatSEQ for Windows Version 4.0
 ; SEQ ID NO: 30
 ; LENGTH: 741
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: fusion protein
 ; US-10-418-836-30

Query Match 98.0%; Score 2716; DB 15; Length 741;
 Best Local Similarity 98.0%; Pred. No. 3.5e-232; Matches 527; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

Qy 1 MSFRSIALSLSVCTGLANVISKRATIDSWISNEATVARTAILNNIGADGAWNSGADSGI 60
 Db 1 MSFRSIALSLSVCTGLANVISKRATIDSWISNEATVARTAILNNIGADGAWNSGADSGI 60

Qy 61 VVASPSTDNPYFYTWRDSDSVLKTVLVDLRNGDTSLSITENYISAQIVQGSNPSG 120
 Db 61 VVASPSTDNPYFYTWRDSDVLVKTLVDLFRNGDTSLSITENYISAQIVQGSNPSG 120

Qy 121 DLSSGAGLGKEKFNDETAVGWSGRPRQDGPAKATAMIGFGQWLDNGYSTATDVW 180
 Db 121 DLSSGAGLGKEKFNDETAVGWSGRPRQDGPAKATAMIGFGQWLDNGYSTATDVW 180

Qy 181 PLVRNDLSYYAQWQYNGTGYDILWEENGSSFTIAVQRALVEGSAFATAVGSSCWDSQ 240
 Db 181 PLVRNDLSYYAQWQYNGTGYDILWEENGSSFTIAVQRALVEGSAFATAVGSSCWDSQ 240

Qy 241 APEILCYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTDPPEACCDSTFQPCSPRALA 300
 Db 241 APEILCYLQSFWTGSPFLANFDSSRSKGDKANTLGSIHTDPPEACCDSTFQPCSPRALA 300

Qy 301 NHKEVUDSFESIYTUNDGLSDSEAVAVGRYPEDTYINGNPWFCLTAAQOLYQWD 360
 Db 301 NHKEVUDSFESIYTUNDGLSDSEAVAVGRYPEDTYINGNPWFCLTAAQOLYQWD 360

Qy 361 KQGSLEVTDSLDFKALYSATGTYSSTSSTYSSIVDAVKTADGFVSIVETHAASNG 420
 Db 361 KQGSLEVTDSLDFKALYSATGTYSSTSSTYSSIVDAVKTADGFVSIVETHAASNG 420

RESULT 14
US-10-418-836-38
; Sequence 38, Application US/10418836
; Publication No. US2004018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Ruaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; FILE REFERENCE: GCT41-2
; CURRENT APPLICATION NUMBER: US/10/418,836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373,889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411,540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452,134
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 38
; LENGTH: 972
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-10-418-836-38

Query Match 98.0%; Score 2715; DB 15; Length 972;
Best Local Similarity 95.5%; Pred. No. 5.8e-232; Mismatches 530; Conservative 0; Indels 21; Gaps 2; Matches 530;

Qy 1 MSFRSLALSGLVCTGLANVISKRATDSLWSNEATVARTAILNNIGADGAWNSGADSGI 60
Db 1 MSFRSLALSGLVCTGLANVISKRATDSLWSNEATVARTAILNNIGADGAWNSGADSGI 60

Qy 61 VVASPSTDNDYFYWTWDSGLVRLKTLVLDLFRNGDTSLSLSTENYISQAIVOGISNSG 120
Db 61 VVASPSTDNDYFYWTWDSGLVRLKTLVLDLFRNGDTSLSLSTENYISQAIVOGISNSG 120

Qy 121 DLSSGAGLGEPKENDETAATGSGRPODGPAKRTAMIGFCWQLDNGYSTADTW 180
Db 121 DLSSGAGLGEPKENDETAATGSGRPODGPAKRTAMIGFCWQLDNGYSTADTW 180

Qy 181 PLVRNDLSVVAQYMNQTYDLMWERVNGSFTIAVORHALVEGSAFATAVGSSCWCSQ 240
Db 181 PLVRNDLSVVAQYMNQTYDLMWERVNGSFTIAVORHALVEGSAFATAVGSSCWCSQ 240

Qy 241 APEILCYQSFWTGSFILANDSFDRSRSGKANTLGSIHFPDPEACDSTFQPCSPRALA 300
Db 241 APEILCYQSFWTGSFILANDSFDRSRSGKANTLGSIHFPDPEACDSTFQPCSPRALA 300

Qy 301 NHKEVWDSFRSYTINDGLSDSEAVAVGRYPEDTYNGNFWFLCTLAABEOLDALYQWD 360
Db 301 NHKEVWDSFRSYTINDGLSDSEAVAVGRYPEDTYNGNFWFLCTLAABEOLDALYQWD 360

Qy 361 KQGSLEVTDVSLDFPKALYSDAVTAGTSSYSSSTSIIDAVKTPADGVSVIETHAASNG 420
Db 361 KQGSLEVTDVSLDFPKALYSDAVTAGTSSYSSSTSIIDAVKTPADGVSVIETHAASNG 420

Qy 421 SMSBQYDKSDGEQLSARDLTWSYALLTANNRRNSVPASWGETSASSVPGTCATSAIG 480
Db 421 SMSBQYDKSDGEQLSARDLTWSYALLTANNRRNSVPASWGETSASSVPGTCATSAIG 480

Qy 481 TYSVTVTWSWPSTIVATGGTTATPTGSSVTSKTTASKS---TTTSGMSL 534
Db 481 TYSVTVTWSWPSTIVATGGTTATPTGSSVTSKTTASKS---TTTSGMSL 534

Qy 525 S-----TTRSGMSL 534
Db 541 SETSLTCTVSGPSL 555

RESULT 15
US-10-418-836-26
; Sequence 26, Application US/10418836
; Publication No. US2004018573A1
; GENERAL INFORMATION:
; APPLICANT: Power, Scott D.
; APPLICANT: Wang, Ruaming
; APPLICANT: Ward, Michael
; TITLE OF INVENTION: Production of Functional Antibodies in
; FILE REFERENCE: GCT41-2
; CURRENT APPLICATION NUMBER: US/10/418,836
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US 60/373,889
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: US 60/411,540
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/452,134
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 60/411,537
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 26
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein
US-10-418-836-26

Query Match 98.0%; Score 2715; DB 15; Length 739;
Best Local Similarity 99.8%; Pred. No. 4.3e-232; Mismatches 522; Conservative 1; Indels 0; Gaps 0; Matches 522;

Qy 1 MSFRSLALSGLVCTGLANVISKRATDSLWSNEATVARTAILNNIGADGAWNSG 60
Db 1 MSFRSLALSGLVCTGLANVISKRATDSLWSNEATVARTAILNNIGADGAWNSG 60

Qy 61 VVASPSTDNDYFYWTWDSGLVRLKTLVLDLFRNGDTSLSLSTENYISQAIVOGISNSG 120
Db 61 VVASPSTDNDYFYWTWDSGLVRLKTLVLDLFRNGDTSLSLSTENYISQAIVOGISNSG 120

Qy 121 DLSSGAGLGEPKENDETAATGSGRPODGPAKRTAMIGFCWQLDNGYSTADTW 180
Db 121 DLSSGAGLGEPKENDETAATGSGRPODGPAKRTAMIGFCWQLDNGYSTADTW 180

Qy 181 PLVRNDLSVVAQYMNQTYDLMWERVNGSFTIAVORHALVEGSAFATAVGSSCWCSQ 240
Db 181 PLVRNDLSVVAQYMNQTYDLMWERVNGSFTIAVORHALVEGSAFATAVGSSCWCSQ 240

Qy 241 APEILCYQSFWTGSFILANDSFDRSRSGKANTLGSIHFPDPEACDSTFQPCSPRALA 300
Db 241 APEILCYQSFWTGSFILANDSFDRSRSGKANTLGSIHFPDPEACDSTFQPCSPRALA 300

Qy 301 NHKEVWDSFRSYTINDGLSDSEAVAVGRYPEDTYNGNFWFLCTLAABEOLDALYQWD 360
Db 301 NHKEVWDSFRSYTINDGLSDSEAVAVGRYPEDTYNGNFWFLCTLAABEOLDALYQWD 360

Qy 361 KQGSLEVTDVSLDFPKALYSDAVTAGTSSYSSSTSIIDAVKTPADGVSVIETHAASNG 420
Db 361 KQGSLEVTDVSLDFPKALYSDAVTAGTSSYSSSTSIIDAVKTPADGVSVIETHAASNG 420

Fri Jun 18 17:42:19 2004

ub-10-038-723-2.rapb

Page 9

Db 361 KQGSLEVDVSLDPFPKALYSRATGYISSSTYSSIVDAWKTFADGFVSVETHASNG 420
Qy 421 SMSEQYDKSDERQSLARDITSYAALITANRRNTPASGETSASSVPTCAATSAIG 480
Db 421 SMSEQYDKSDERQSLARDITSYAALITANRRNTPASGETSASSVPTCAATSAIG 480
Qy 481 TYSSVTVTSWISIVATGTTTATPGSGSTTSKTTAASK 523
Db 481 TYSSVTVTSWISIVATGTTTATPGSGSTTSKTTAASK 523

Search completed: June 17, 2004, 17:53:29
Job time : 51 secs

L115
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OM Protein - protein search, using sw model
Run on: June 17, 2004, 17:44:49 ; Search time 23 Seconds
(Without alignments)

Perfect score: US-10-038-723-2
Sequence: 1 MSFRSLALSGLVCTGLANV.....SKTTATASKTSTTRSGMSL 534
Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched:

389414 seqs, 5162571 residues
Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA,*
1: /cgn2_6_ptodata/21aa/5A_COMB_pep_*
2: /cgn2_6_ptodata/21aa/5B_COMB_pep_*
3: /cgn2_6_ptodata/21aa/6A_COMB_pep_*
4: /cgn2_6_ptodata/21aa/6B_COMB_pep_*
5: /cgn2_6_ptodata/21aa/PCITS_COMB_pep_*
6: /cgn2_6_ptodata/21aa/backfilesl_pep:_*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2771	100.0	534	3 US-09-198-672-2
2	2771	100.0	534	3 US-09-199-290-9
3	2771	100.0	534	4 US-09-632-392-2
4	2771	100.0	534	4 US-09-455-679-1
5	2771	100.0	534	4 US-09-351-814-2
6	2771	100.0	534	4 US-09-821-616-9
7	2742	97.0	640	4 US-09-351-814-13
8	2628	94.8	616	4 US-09-236-063-1
9	1689	61.0	618	3 US-09-199-290-34
10	1689	61.0	618	4 US-09-821-616-34
11	1674.5	60.4	591	3 US-09-199-290-7
12	1674.5	60.4	591	4 US-09-821-616-7
13	1615.5	58.3	630	4 US-09-704-449-2
14	1577	56.9	626	2 US-09-596-300A-7
15	1577	56.9	626	2 US-09-596-300A-14
16	1425.5	51.4	581	4 US-09-534-407-3
17	1425.5	51.4	581	4 US-09-534-407-3
18	1321	47.7	616	1 US-08-385-370-2
19	1321	47.7	616	1 US-08-385-370-4
20	589	21.3	806	1 US-08-070-67A-11
21	160	5.8	35	3 US-09-199-290-4
22	160	5.8	35	4 US-09-821-616-4
23	156.5	5.6	2137	4 US-09-134-001C-463
24	142	5.1	536	4 US-09-463-712C-10
25	136	4.9	1026	2 US-08-614-377A-7
26	136	4.9	1026	3 US-09-142-648B-7
27	133			

RESULT 1
US-09-198-672-2
; Sequence 2, Application US/09198672
; Patent No. 6129788
; GENERAL INFORMATION:
; APPLICANT: Liaw, Gin
; APPLICANT: Pedersen, Sven
; APPLICANT: Hendriksen, Sven
; TITLE OF INVENTION: A Method of Producing Saccharide
; FILE REFERENCE: 5318.200-US
; CURRENT APPLICATION NUMBER: US/09/198, 672
; CURRENT FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSBQ for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Aspergillus Niger
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; US-09-198-672-2

Query Match 100.0%; Score 2771; DB 3; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-231; Mismatches 0; Indels 0; Gaps 0;

Matches 534; Conservative 0; Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
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Sequence 61, VVASRSTDNDYFYWTDRDGLVKTIVLWDLFRNGDTSLISTENIQAIVQGTSNPSG
Db 61 VVASRSTDNDYFYWTDRDGLVKTIVLWDLFRNGDTSLISTENIQAIVQGTSNPSG
Qy 61 VVASRSTDNDYFYWTDRDGLVKTIVLWDLFRNGDTSLISTENIQAIVQGTSNPSG
Qy 121 DLSSGAGLGPBKFNEDTAVTGSNRPDRGPALRATAMIGSOWLNGYTSTATDW 180
Db 121 DLSSGAGLGPBKFNEDTAVTGSNRPDRGPALRATAMIGSOWLNGYTSTATDW 180
Qy 181 PLVRNDLSYQXQNYQTGYDLWEVNGSSFTIAVORHALVESSAFATAVGSSCWCSQ 240
Db 181 PLVRNDLSYQXQNYQTGYDLWEVNGSSFTIAVORHALVESSAFATAVGSSCWCSQ 240
Qy 301 NHKEVUDSRSIYLTFLDGLSDSEVAVARYPEDTYNNPWPFLCTLAQAEQLDLYWD 360
Db 301 NHKEVUDSRSIYLTFLDGLSDSEVAVARYPEDTYNNPWPFLCTLAQAEQLDLYWD 360

Db 301 NHKEVUDSPRSIYTINDGSDSEAVAVGRYPEDTYINGNPWFCLTLAAEQDLYQMD 360
 Qy 361 KQGSLEVTVSLDFKALYSDAATGTYSSSSTSSIVDAVKTFADGFSIVETHAASNG 420
 Db 361 KQGSLEVTVSLDFKALYSDAATGTYSSSSTSSIVDAVKTFADGFSIVETHAASNG 420
 Qy 421 SMSQYQDSGEOLSDARDLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAIG 480
 Db 421 SMSQYQDSGEOLSDARDLTWSYALLTANRNRNSVPASWGETSASSVPGTCATSAIG 480
 Qy 481 TYSVTVTSPSPSIATGGTTATPTGSSVTSKTTASKSTTRSGMSL 534
 Db 481 TYSVTVTSPSPSIATGGTTATPTGSSVTSKTTASKSTTRSGMSL 534
RESULT 2
 US-09-159-290-9
 ; Sequence 9, Application US/09199290
 ; Patent No. 6255084
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Birne R.
 ; APPLICANT: Nielsen, Ruby
 ; APPLICANT: Lehmbbeck, Jan
 ; TITLE OF INVENTION: Thermostable Glucoamylase
 ; FILE REFERENCE: 5279 200-US
 ; CURRENT APPLICATION NUMBER: US/09/199, 290
 ; CURRENT FILING DATE: 1998-11-24
 ; EARLIER APPLICATION NUMBER: 1557/97
 ; EARLIER FILING DATE: 1997-12-30
 ; EARLIER APPLICATION NUMBER: 0225/98
 ; EARLIER FILING DATE: 1998-07-10
 ; EARLIER APPLICATION NUMBER: 60/070, 746
 ; EARLIER FILING DATE: 1998-01-08
 ; EARLIER APPLICATION NUMBER: 60/094, 344
 ; EARLIER FILING DATE: 1998-07-28
 ; EARLIER APPLICATION NUMBER: 08/979, 673
 ; EARLIER FILING DATE: 1997-11-26
 ; EARLIER APPLICATION NUMBER: 09/017, 657
 ; EARLIER FILING DATE: 1998-06-30
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
US-09-159-290-9
 Query Match 100.0%; Score 2771; DB 3; Length 534;
 Best Local Similarity 100.0%; Pred. No. 1.1e-231; Gaps 0;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFRSLAISGLVCTGLANVSKRATLDSMSLNBEATVARTAILNNIGAGAWGAGSGI 60
 Db 1 MSFRSLAISGLVCTGLANVSKRATLDSMSLNBEATVARTAILNNIGAGAWGAGSGI 60
 Qy 61 WVASPSTDNDPYFTWTRDGLVLUKTVDLFRNGDTSLISTINYISAQAVQGISNSG 120
 Db 61 WVASPSTDNDPYFTWTRDGLVLUKTVDLFRNGDTSLISTINYISAQAVQGISNSG 120
 Qy 1 MSFRSLAISGLVCTGLANVSKRATLDSMSLNBEATVARTAILNNIGAGAWGAGSGI 60
 Db 1 MSFRSLAISGLVCTGLANVSKRATLDSMSLNBEATVARTAILNNIGAGAWGAGSGI 60
 Qy 61 WVASPSTDNDPYFTWTRDGLVLUKTVDLFRNGDTSLISTINYISAQAVQGISNSG 120
 Db 61 WVASPSTDNDPYFTWTRDGLVLUKTVDLFRNGDTSLISTINYISAQAVQGISNSG 120
 Qy 121 DLSGAGLGEPKFNDEATYGSWGRPRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Db 121 DLSGAGLGEPKFNDEATYGSWGRPRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Qy 241 APEILCYQSFWMGSFILANDFDSSRGKDANTLGSITFEDPEACDDSTFQCPSPRALA 300
 Db 241 APEILCYQSFWMGSFILANDFDSSRGKDANTLGSITFEDPEACDDSTFQCPSPRALA 300
 Qy 181 PLVRNDLSVVAQYWNQGTYDMLWEBNGSFFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240
 Db 181 PLVRNDLSVVAQYWNQGTYDMLWEBNGSFFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240
 Qy 241 APEILCYQSFWMGSFILANDFDSSRGKDANTLGSITFEDPEACDDSTFQCPSPRALA 300
 Db 241 APEILCYQSFWMGSFILANDFDSSRGKDANTLGSITFEDPEACDDSTFQCPSPRALA 300
 Qy 301 NHKEVUDSPRSIYTINDGSDSEAVAVGRYPEDTYINGNPWFCLTLAAEQDLYQMD 360
 Db 301 NHKEVUDSPRSIYTINDGSDSEAVAVGRYPEDTYINGNPWFCLTLAAEQDLYQMD 360
RESULT 3
 US-09-632-392-2
 ; Sequence 2, Application US/09632392
 ; Patent No. 6303346
 ; GENERAL INFORMATION:
 ; APPLICANT: Liaw, Gin
 ; APPLICANT: Pedersen, Sven
 ; APPLICANT: Hendriksen, Sven
 ; TITLE OF INVENTION: A Method of Producing Saccharide
 ; TITLE OF INVENTION: Preparations
 ; FILE REFERENCE: 5318 200-US
 ; CURRENT APPLICATION NUMBER: US/09/632, 392
 ; CURRENT FILING DATE: 2000-01-04
 ; PRIOR APPLICATION NUMBER: 09/198, 672
 ; PRIOR FILING DATE: 1998-11-23
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 534
 ; TYPE: PRT
 ; ORGANISM: Aspergillus Niger
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: (1)...(24)
US-09-632-392-2
 Query Match 100.0%; Score 2771; DB 4; length 534;
 Best Local Similarity 100.0%; Pred. No. 1.1e-231; Gaps 0;
 Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSFRSLAISGLVCTGLANVSKRATLDSMSLNBEATVARTAILNNIGAGAWGAGSGI 60
 Db 1 MSFRSLAISGLVCTGLANVSKRATLDSMSLNBEATVARTAILNNIGAGAWGAGSGI 60
 Qy 61 WVASPSTDNDPYFTWTRDGLVLUKTVDLFRNGDTSLISTINYISAQAVQGISNSG 120
 Db 61 WVASPSTDNDPYFTWTRDGLVLUKTVDLFRNGDTSLISTINYISAQAVQGISNSG 120
 Qy 121 DLSGAGLGEPKFNDEATYGSWGRPRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Db 121 DLSGAGLGEPKFNDEATYGSWGRPRDGPA RATAMIGFCWMLDNGYSTADIW 180
 Qy 241 APEILCYQSFWMGSFILANDFDSSRGKDANTLGSITFEDPEACDDSTFQCPSPRALA 300
 Db 241 APEILCYQSFWMGSFILANDFDSSRGKDANTLGSITFEDPEACDDSTFQCPSPRALA 300
 Qy 301 NHKEVUDSPRSIYTINDGSDSEAVAVGRYPEDTYINGNPWFCLTLAAEQDLYQMD 360
 Db 301 NHKEVUDSPRSIYTINDGSDSEAVAVGRYPEDTYINGNPWFCLTLAAEQDLYQMD 360

RESULT 4
US-09-455-679-1
; Sequence 1, Application US/09455679
; Patent No. 6329186
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne R.
; APPLICANT: Svendaen, Allan
; APPLICANT: Bojsen, Kristian
; APPLICANT: Vind, Jesper
; APPLICANT: Pedersen, Henrik
; TITLE OF INVENTION: Glucoamylases with N-Terminal Extensions
; CURRENT APPLICATION NUMBER: US/09/455, 679
; CURRENT FILING DATE: 1999-12-07
; EARLIER APPLICATION NUMBER: PA 1998 01616
; EARLIER FILING DATE: 1998-12-07
; EARLIER APPLICATION NUMBER: PA 1999 00409
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/111, 674
; EARLIER FILING DATE: 1998-12-10
; EARLIER APPLICATION NUMBER: 60/126, 740
; EARLIER FILING DATE: 1999-03-29
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; US-09-455-679-1

Query Match 100.0%; Score 2771; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-231; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFRSLLAISGLCGLVCTGLANVIKSKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGI 60
Db 1 MSFRSLLAISGLCGLVCTGLANVIKSKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGI 60
QY 61 VVASPSTDNPDYFYTWTRDGLVLKTKLVLDFRNGDTSLISTENIYISAQIVQG1SNPSG 120
Db 1 VVASPSTDNPDYFYTWTRDGLVLKTKLVLDFRNGDTSLISTENIYISAQIVQG1SNPSG 120
QY 121 DLSSGAGLGKPKENDETAVTGSWGRQRQDGPAKATAMIGFGQWLDNGYSTATDIW 180
Db 121 DLSSGAGLGKPKENDETAVTGSWGRQRQDGPAKATAMIGFGQWLDNGYSTATDIW 180
QY 181 PLVRDLSYYAQYWNQTYDIMEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Db 181 PLVRDLSYYAQYWNQTYDIMEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
QY 241 APEIICYLQSFMTGSPILANDDSRSRGKDANTLGLSIIHDPPEACDDSTFQCPSPRALA 300
Db 241 APEIICYLQSFMTGSPILANDDSRSRGKDANTLGLSIIHDPPEACDDSTFQCPSPRALA 300
QY 301 NHKEVVDSPRSIYTUNDGLSDESEAVALGRPEPTYNGNPWFCLTLAAQOLYDALYQWD 360
Db 301 NHKEVVDSPRSIYTUNDGLSDESEAVALGRPEPTYNGNPWFCLTLAAQOLYDALYQWD 360

RESULT 5
US-09-351-814-2
; Sequence 2, Application US/09351814
; Patent No. 632851
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Bjarne Roenfeldt
; APPLICANT: Svendaen, Allan
; APPLICANT: Pedersen, Henrik
; APPLICANT: Vind, Jesper
; APPLICANT: Hendriksen, Hanne Vang
; TITLE OF INVENTION: Glucoamylase Variants
; FILE REFERENCE: 5636_200-US
; CURRENT APPLICATION NUMBER: US/09/351, 814
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: PA 1998 00937
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PA 1998 01667
; EARLIER FILING DATE: 1998-12-17
; EARLIER APPLICATION NUMBER: 60/093, 528
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/115, 545
; EARLIER FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(24)
; US-09-351-814-2

Query Match 100.0%; Score 2771; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-231; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSFRSLLAISGLCGLVCTGLANVIKSKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGI 60
Db 1 MSFRSLLAISGLCGLVCTGLANVIKSKRATLDSWLSNEATVARTAILNNIGADGAWVSGADSGI 60
QY 61 VVASPSTDNPDYFYTWTRDGLVLKTKLVLDFRNGDTSLISTENIYISAQIVQG1SNPSG 120
Db 61 VVASPSTDNPDYFYTWTRDGLVLKTKLVLDFRNGDTSLISTENIYISAQIVQG1SNPSG 120
QY 121 DLSSGAGLGKPKENDETAVTGSWGRQRQDGPAKATAMIGFGQWLDNGYSTATDIW 180
Db 121 DLSSGAGLGKPKENDETAVTGSWGRQRQDGPAKATAMIGFGQWLDNGYSTATDIW 180
QY 181 PLVRDLSYYAQYWNQTYDIMEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
Db 181 PLVRDLSYYAQYWNQTYDIMEENGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
QY 241 APEIICYLQSFMTGSPILANDDSRSRGKDANTLGLSIIHDPPEACDDSTFQCPSPRALA 300
Db 241 APEIICYLQSFMTGSPILANDDSRSRGKDANTLGLSIIHDPPEACDDSTFQCPSPRALA 300
QY 301 NHKEVVDSPRSIYTUNDGLSDESEAVALGRPEPTYNGNPWFCLTLAAQOLYDALYQWD 360
Db 301 NHKEVVDSPRSIYTUNDGLSDESEAVALGRPEPTYNGNPWFCLTLAAQOLYDALYQWD 360

RESULT 6
US-09-821-616-9
; Sequence 9, Application US/09821616
; Patent No. 6620324

GENERAL INFORMATION:
APPLICANT: Nielsen, Bjarne R.
APPLICANT: Nielsen, Ruby
APPLICANT: Leimbekk, Jan
TITLE OF INVENTION: Thermostable Glucoamylase
FILE REFERENCE: 5279_200-US
CURRENT APPLICATION NUMBER: US/09/821,616
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/199,290
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 9
LENGTH: 534
TYPE: PRT
ORGANISM: Aspergillus niger
FEATURE:
LOCATION: (1)...(24)
US-09-821-616-9

Query Match 100.0%; Score 2771; DB 4; Length 534;
Best Local Similarity 100.0%; Pred. No. 1.1e-231; Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDSGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDSGI 60

QY 61 WVASPSTDNPDYFVWTROSGLVCTVLDFRNGDTSLISTIENYISAQIYOGISNSPG 120
Db 61 WVASPSTDNPDYFVWTROSGLVCTVLDFRNGDTSLISTIENYISAQIYOGISNSPG 120

QY 121 DLSSGAGLGEPKENDETAVTGSWGRPDRDPALRATAMIGFCQWLNDNGYSTATDHW 180
Db 121 DLSSGAGLGEPKENDETAVTGSWGRPDRDPALRATAMIGFCQWLNDNGYSTATDHW 180

QY 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240
Db 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240

QY 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240
Db 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240

QY 241 APEIUCYLOSFWSFILANDFSSRSKGQDANTLGSINTFPEACDDSTFOPCSPRALA 300

RESULT 7
US-09-351-814-13
; Sequence 13, Application US/09351814
; Patent No. 6352851

GENERAL INFORMATION:
APPLICANT: Nielsen, Bjarne Roenfeldt
APPLICANT: Svendsen, Allan
APPLICANT: Pedersen, Henrik
APPLICANT: Vind, Jesper
APPLICANT: Hendriksen, Hanne Vang
APPLICANT: Frandsen, Torben Peter
TITLE OF INVENTION: Glucoamylase Variants
FILE REFERENCE: 5636_200-US
CURRENT APPLICATION NUMBER: US/09/351,814
CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: PA 1998 00337
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: PA 1998 01667
EARLIER FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: 60/093,528
EARLIER FILING DATE: 1998-07-21
EARLIER APPLICATION NUMBER: 60/115,545
EARLIER FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO: 13
LENGTH: 640
TYPE: PRT
ORGANISM: ASPERGILLUS NIGER
LOCATION: (1)...(13)
US-09-351-814-13

Query Match 99.0%; Score 2742; DB 4; Length 640;
Best Local Similarity 99.6%; Pred. No. 4.9e-229; Matches 528; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDSGI 60
Db 1 MSFRSLLAISGLVCTGLANVISKRATLDSWLSNEATVARTAILNNIGADGAWGAGDSGI 60

QY 61 WVASPSTDNPDYFVWTROSGLVCTVLDFRNGDTSLISTIENYISAQIYOGISNSPG 120
Db 61 WVASPSTDNPDYFVWTROSGLVCTVLDFRNGDTSLISTIENYISAQIYOGISNSPG 120

QY 121 DLSSGAGLGEPKENDETAVTGSWGRPDRDPALRATAMIGFCQWLNDNGYSTATDHW 180
Db 121 DLSSGAGLGEPKENDETAVTGSWGRPDRDPALRATAMIGFCQWLNDNGYSTATDHW 180

QY 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240
Db 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240

QY 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240
Db 181 PLVRNDLSYVAQWMQTYGILWEENGSSFTIAVORHALVEGSAFATAVGSSCSWCDSQ 240

QY 241 APEIUCYLOSFWSFILANDFSSRSKGQDANTLGSINTFPEACDDSTFOPCSPRALA 300

Db 241 APFILCVLQSFPTGFSFLANDPSSRGKDANVLLGSIHTFPPEAACDDSTPQCPSPRALA 300
 Qy 301 NHKEVUDSFRSYTLYNDGLSSEA VAVGRYEPDTYNGNPFLCTLAAGQDLYQMD 360
 Db 301 NHKEVUDSFRSYTLYNDGLSSEA VAVGRYEPDTYNGNPFLCTLAAGQDLYQMD 360
 Qy 361 KQGSLEVTDVASDFKALYSRATGYSSSTYSSIVDAWKTFRADGFVSTVETHASNG 420
 Db 361 KQGSLEVTDVASDFKALYSRATGYSSSTYSSIVDAWKTFRADGFVSTVETHASNG 420
 Qy 421 SNEQDQDKSDQBLQSLARDLTWSYAAUJNTANNRNSVPASWGETSASSVRCAATSAIG 480
 Db 421 SNEQDQDKSDQBLQSLARDLTWSYAAUJNTANNRNSVPASWGETSASSVRCAATSAIG 480
 Qy 481 TYSVSVTWSWPSIVATGGTTATPTGSGSYTSKTKTATASKTSSTSS 530
 Db 481 TYSVSVTWSWPSIVATGGTTATPTGSGSYTSKTKTATASKTSSTSS 530

RESULT 9
 US-09-236-063-1
 Sequence 1, Application US/09236063
 Patent No. 6533792

GENERAL INFORMATION:

- APPLICANT: Allen, Martin
- APPLICANT: Fang, Teuei-Yun
- APPLICANT: Li, Yuxing
- APPLICANT: Liu, Hsuan-Liang
- APPLICANT: Chen, Hui-Mei
- APPLICANT: Coutinho, Pedro
- APPLICANT: Hanzakor, Richard
- APPLICANT: Ford, Clark

TITLE OF INVENTION: PROTEIN ENGINEERING OF GLUCOMYLASE TO INCREASE PH OPTIMUM, SUBSTRATE SPECIFICITY AND THERMOSTABILITY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Kohn & Associates
 STREET: 30500 No. 653792thwestern Hwy.
 CITY: Farmington Hills
 STATE: Michigan
 COUNTRY: US
 ZIP: 48334

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/236,063
 FILING DATE: CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Kohn, Kenneth I.
 REGISTRATION NUMBER: 30,955
 REFERENCE/DOCKET NUMBER: 0812.00001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (248) 533-5050
 TELEFAX: (248) 539-5055

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

- LENGTH: 616 amino acids
- TYPE: amino acid
- STRANDNESS: single
- TOPOLOGY: linear
- MOLECULE TYPE: protein
- HYPOTHETICAL: NO
- ORIGINAL SOURCE: ORGANISM: Aspergillus

US-09-236-063-1

Query Match 94.0%; Score 2628; DB 4; Length 616;
 Best Local Similarity 99.6%; Pred. No. 3.5e-219;

RESULT 9
 US-09-199-290-34
 Sequence 34, Application US/09199290
 Patent No. 6255084

GENERAL INFORMATION:

- APPLICANT: Nielsen, Bjarne R.
- APPLICANT: Nielsen, Ruby
- APPLICANT: Lehnebeck, Jan

TITLE OF INVENTION: Thermostable Glucoamylase

FILE REFERENCE: 5279-200-US

CURRENT APPLICATION NUMBER: US/09/199,290
 CURRENT FILING DATE: 1998-11-24
 EARLIER APPLICATION NUMBER: 1557/97

EARLIER FILING DATE: 1997-12-30
 EARLIER APPLICATION NUMBER: 0925/98
 EARLIER FILING DATE: 1998-07-10
 EARLIER APPLICATION NUMBER: 60/070,746
 EARLIER FILING DATE: 1998-01-08
 EARLIER APPLICATION NUMBER: 60/094,344
 EARLIER FILING DATE: 1998-07-28
 EARLIER APPLICATION NUMBER: 08/979,673
 EARLIER FILING DATE: 1997-11-26
 EARLIER APPLICATION NUMBER: 09/107,657
 EARLIER FILING DATE: 1998-06-30
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 34
 LENGTH: 618
 TYPE: PRT
 ORGANISM: Talaromyces emersonii

US-09-199-290-34

Query Match 61.0%; Score 1689; DB 3; Length 618;
 Best Local Similarity 61.2%; Pred. No. 9.1e-138;

Query Match 60.4%; Score 1674.5; DB 3; Length 591;
 Best Local Similarity 62.3%; Pred. No. 1.5e-136; Mismatches 314; Conservative 73; Mismatches 102; Index 15; Gaps 3;

Qy 26 TLDWSIISNEATVARTAILNNITGADGAWNSGAGSIWVASPSTNDNPYFTWTRDSGLVLK 85
 Db 4 SLDSFLATEPTIALQGVNLNIGPNGADVAGASAGIVVASPSPRSRDPNPFYSWTRDAALTAK 63

Qy 86 TLVDLFRNGDPLSLSTENYSAQAVOGISNPSCDLSAGLGKEPKFNTDETAYGSWG 145
 Db 64 YLVDAFNRRGNKDLQEQTQYIQAQKVOTISNPSGLSTG-GLGEPKFNVETAFGPWG 122

Qy 146 RPQRDGPAKTRAMIGFGQMLDNGYSTATDIWPLVRNDSYVAQYWNQTYGDIWEV 205
 Db 123 RQQRDGPAKTRALIAVANYLIDNGEASTABDIIMPVONLISYTOYWNSTFDIWEV 182

Qy 206 NGSSFTTAOVRALVEGSAPATAVESCSWCDSDQAPBILCYLOSFWTGSGTIANH-DSS 264
 Db 183 EGSSFFTAVQHRLAEGNALATRINTCNSCVSOPQVLCFLQSFTWGSVLANFGGSG 242

Qy 243 RSKGDVNSILSISIHTFDPAGECDSTFOPCSARALARANKVVTDSFRSIYAINSGIAEGSA 302
 Db 325 VAVGRYPEDTYNGNPWFLCTLAEEQLYDQYQWDQGSLEVTVDYSLDFERKALYDAAT 384
 Db 303 VAVGRYPEDVYOGGNPYLATAAAQOLYDAYQWIKIGSISITDVSLLPFDIYSAV 362

Qy 385 GRYSSSSSTYVSIIDAVKTFADGFVSVIETVHASNGSMSYDQKSGEOQSARDITWSYA 444
 Db 363 GTYNSSSTTENDISIAVQTYGGLVLSVERKTPSDGTSRDPSPRSRDGTPLUSALTWSYA 422

Qy 445 ALLTANRNRNSVUPASWGETBASSVPCATSAIGYSSVTVSPSIVATGGTTTAT 504
 Db 423 SILTASARROSVUPASWGEASSVLAVCATSATGPYSTATNTWPS----- 470

Qy 505 PTGGSVTSKTTASKTSTT 528
 Db 471 -SGSGSSTTSAAPCTPTSVAVT 493

RESULT 12

US-09-821-616-7
 ; Sequence 7, Application US/09821616
 ; Patent No. 6620924
 ; GENERAL INFORMATION:
 ; APPLICANT: Nielsen, Bjarne R.
 ; APPLICANT: Nielsen, Bjarne R.
 ; APPLICANT: Lembeck, Jan
 ; TITLE OF INVENTION: Thermostable Glucoamylase
 ; FILE REFERENCE: 5279-200-US
 ; CURRENT APPLICATION NUMBER: US/09/821,616
 ; CURRENT FILING DATE: 2001-03-29
 ; CURRENT APPLICATION NUMBER: 09/199,290
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-24
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 1557/97
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 0925/98
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,746
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-08
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/094,344
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-28
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/979,673
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-26
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/107,657
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-30
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; LENGTH: 591
 ; TYPE: PRT
 ; ORGANISM: Talaromyces emersonii

RESULT 13

US-09-704-449-2
 ; Sequence 2, Application US/09704449
 ; Patent No. 6309872
 ; GENERAL INFORMATION:
 ; APPLICANT: Rey, Michael W.
 ; APPLICANT: Goilghtly, Elizabeth J.
 ; TITLE OF INVENTION: Polypeptides Having Glucoamylase
 ; TITLE OF INVENTION: Activity And Nucleic Acid Encoding Same
 ; FILE REFERENCE: 10101.000-US
 ; CURRENT APPLICATION NUMBER: US/09/704,449
 ; CURRENT FILING DATE: 2000-11-01
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 630
 ; TYPE: PRT
 ; ORGANISM: Thielavia terrestris

US-09-704-449-2

Query Match 58.3%; Score 1615.5; DB 4; Length 630;
 Best Local Similarity 58.9%; Pred. No. 2.2e-131; Mismatches 315; Conservative 83; MisMatches 112; Index 25; Gaps 7;

Qy 6 LIALSGLCIVCTGLANVTKRA-----TLDWSIISNEATVARTAILNNITGADGAWNSGAG 56
 Db 6 LIGLIALPAIGHPEASRVREGEVVKRSVDSFATESPIALSNUCLIGSTGHASGV 65

Qy 57 DSGIWAASPTNDNPYFTWTRDSLVLKTLVDFRNQ-DTSLISTIENYSAQAVIYQGI 115

Db 65 ASGIVVASSPDKTKNDYWMYPTWDSALTICKVWDFTINSASLQAEIQYIVQAHLGGV 125
 Qy 116 SNRPGDLSSGAAGLGEPRPKENVDETAYTGSNGR PORDGPALARATAMIGFCQWLNDGYSTA 175
 Db 126 SNPSSGLSDGSGLGEPKPNVMSOFTGANGRPPORDGPALARAIJAYSKWILISNGYSTA 185
 Qy 176 DTIWPLVNLDSLTYAQYMNQTCYLWEEVNGSRSFTAVQRHALVESAFATAVGSCS 235
 Db 186 SSIWPKNDLWATYAO - NNTGFDLWEEVGSSPFTVANORALVEGALATSLGTSCS 243
 Qy 236 WCDSQAPELCLYQSPWIGS - FFLANFDSRSKQDANTLGSHTPDEAACDSTQP 293
 Db 244 ACSAVAPOLICFLQSFWSPSGYTLAN---STAKDANTLGSHTPDEAACDSTQP 299
 Qy 294 CSPRALANIKETVVDSPRSIYTLDGLSDBAVAVGVRYPDTYNGNPWFCLTLAAEOLY 353
 Db 300 CSDRALANIKVTDFAFRSYISNSGIAEGSAVAVGRYPDSYFGGNPWFCLTLAAEOLY 359
 Qy 354 DALYQDKGSLTVDSDPFKALYSDAATGTYSSSSTYSSITDAVKTFAFGFVSTE 413
 Db 360 DALYWKKQCSSTVTVSTLAFKFQFSSSITPGTYSSTTLYNALISAYADGCMNTVA 419
 Qy 414 THAASNQNSSEQYQKSDGQLSARDLTWSYALLTANNRNSVUPASNGETSSAVPGTC 473
 Db 420 YQAGTNGSLSQFSKTINGERPLSAYDLTWSYAFLTAARRAGVUPPSNGAASANSVPAC 479
 Qy 474 ATAAIGTGSSTVTSWPSIVATGTTTATPTGGSVSTSKTTASKTST 528
 Db 480 SATSVGVSYSATATSFP-----SQTFASTSGS SPASSATATACTSP 527

RESULT 14
 US-08-536-300A-7
 ; Sequence 7, Application US/08596300A
 ; Patent No. 5,834,919
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT:
 ; TITLE OF INVENTION: Production of Heterologous Peptides
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/596,300A
 FILING DATE: 13-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1321-1-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800
 TELEFAX: 201 343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 626 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:

RESULT 15
 US-08-596-300A-14
 ; Sequence 14, Application US/08596300A
 ; Patent No. 5,834,919
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT:
 ; TITLE OF INVENTION: Production of Heterologous Peptides
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/596,300A
 FILING DATE: 13-FEB-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 1321-1-001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201 487-5800

Query Match 56.9%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 4,8e-18;
 Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;

Db 13 AFQAVLGPDPPLHEKRHSDDIKR-SVDSYIQETPIAQOKNLONGASCGRASGAGSV 71
 Db 18 VASPTDIDPYKWTWTRSLVLUKTLVLFRING-DTSILISTIENYIYQATYOGISNSG 120
 Db 22 VASESKSPPDYWTWTRSLVLUKTLVLFRING-DTSILISTIENYIYQATYOGISNSG 131
 Db 121 DLSSGAGLGEPKENVDETAYTGSNGR PORDGPALARATAMIGFCQWLNDGYSTA 180
 Db 132 SLNGAGLGEPKENVDLQFTGAWGRQRDGPPLARALIGYKWLWNGYADTAKSIIW 191
 Db 181 PLVRLNDLSYVAQWQNQTSYDYLWEEVNGSSEFTIAVQRHALVESAFATAVGSCSWCDSQ 240
 Db 192 PIVKDIALYTAQWNTFDFLWEEVNSSSFTIAASHRHALVESAFAKVGSCSACDAI 251
 Db 241 APEIICLYQSPWIGS - FFLANFDSRSKQDANTLGSHTPDEAACDSTQPSCPRL 299
 Db 252 APOIICFQDFQFWSNWSGYLISNFYRSDKINDVLSHTNFDPAAGCIVNTIOPCPRL 311
 Db 300 ANHKEWVUSFRSITYLNDGLSDSEAVAVGRYPDTYNGNPWFCLTLAAEOLYDALYQW 359
 Db 312 ANHKVWVUDSMR-FWGVNNGRTAGKAAYAVGRYADEVYNGNPWFCLTLAAEOLYDVW 370
 Db 360 DKQGSLETDVSDPFKALYSDAATGTYSSSSTYSSITDAVKTFAFGFVSTE 419
 Db 371 KKQOSITVTISLAFKOLPVPSVTGTTSSSTYTAIINVITYAOGFVDIAQYTPSD 430
 Db 420 GSMEQYKSDGQLSARDLTWSYALLTANNRNSVUPASNGETSSAVPGTCATSAI 479
 Db 431 GSIAEQPKDGSAPLSTHLTWSYASFFSAARRAGVUPPSNGAASANSLPGSCSASTVA 490
 Qy 480 GTYSSVTWPSIVATGTTT-ATPTGGS---VTSKTTASKT 524
 Db 491 GSYATATATSFPANLTPASTTVRPPTQGCACDHEVLVTFNEKVTSYGOT 541

TELE: 133521
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 626 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 FRAGMENT TYPE:
 US-08-596-300A-14

Query Match 56.9%; Score 1577; DB 2; Length 626;
 Best Local Similarity 57.6%; Pred. No. 4.8e-128; Mismatches 6;
 Matches 306; Conservative 85; MisMatches 130; Indels 10; Gaps 6;
 Query 2 SFRLSLLALSGIVCTGLANLVIKRATUDSWLNEATVARTATLNNIGADGAWVGADSGIV 61
 Db 13 AFQAVLGLIPDHLERKRHSIDIKR-SDSYIQTETPIAQKNLICNIGSGCRAASGAAGVV 71
 Query 62 VASPSTINPPDFYTWRDSGIVLKTLVDLFENG-DISLSLTENYISAQAVQGVSNSPG 120
 Db 72 VASPKSKSPDYWTWTRDAALVTKLIVDEFNDYNTLQNTQAOYAAQAKLQGVSNPSG 131
 Query 121 DLSSGAGLGERKFNDETAVGSWGRQDGPALARATAMIGFGQWLUDNGYSTATDIW 180
 Db 132 SLSNGAGLGERKFMVLQDFGAWGRQDGPPLRALIGYGKWIUSVNGADTAKSIW 191
 Query 181 PLVRNDISYVQYWNQTYGDIDWEEVNGSSFTIAVORHALVEGSAFATAVGSSCWCDSQ 240
 Db 192 PIVKNDIAYTQIWNNGFDIWEEVNVSFFTTIASHRHALVEGSAFKSVSSCSACDAI 251
 Query 241 APEILCYLQSFSTWIGS-FILANFDSSRSQKDANTLGSIHTDPPEAACDPSFQPSPRAL 299
 Db 252 APOILCFQOSFWNSNGYIISNFVNVRSGKDINSVLTSHNFDPAAGCDVNTFQPCSDRAL 311
 Query 300 ANHKEVUDSFHSITYLNDGLSSEAVAVGRYPEDTYINGNPFCLIAAEQLYDIALW 359
 Db 312 ANHKVUVVDSMR-FWGUNSGRAGKAAGAVGRFAEDVYNGNWYLATLAABQLYDVW 370
 Query 360 DKQGSLEVTDVSLDFKALYSDAATGTYSSSSSTVSSIUDVVKTFADGFYVSIVETHASN 419
 Db 371 KKQGSITVTSISLAFFKDLVSVSIVGTYSSSSSTYTAIINATTIADGFVDIVAQTPSD 430
 Query 420 GSMSEGYDKSGEQLSARDIWTSYAALLTANRNSVUPASWGETSASSVPGTCATSAI 479
 Db 431 GSIAEOPDKDQGAPLSATHLWMSYASFLSAARRAGIVPPSGAASANSLPGSCASTVA 490
 Query 480 GTYSSTVTSPSPSIVATGGTTT-ATPTGSSS----VTSTSQTATASKT 524
 Db 491 GSYATATATSPANLTPASTTVTPPPQRTGCAADHEVLTIFNEKVITSYGGT 541

Search completed: June 17, 2004, 17:48:36
 Job time : 25 SECs

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OM protein - protein search, using SW model

Run on:

June 17, 2004, 17:42:38 ; Search time 46 Seconds

(without alignments)

3662.755 Million cell updates/sec

Title: US-10-038-723-2
Perfect score: 2771

Sequence: 1 MSFRSLIALSGLVCTGIANV.....SKTTATASKTSTTRSCMSL 534

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPIREMBI_25 : *
1: sp_archea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_micr: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp Rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

* Query Match Length DB ID Description

Result No.	Score	Match	Length	DB ID	Description
1	2669.5	95.3	639	3 Q870GB	Q870GB aspergillus
2	2564.5	92.5	639	3 Q12537	Q12537 aspergillus
3	1689	61.0	618	3 Q9CIV4	Q9CIV4 talaromycetes
4	1518	54.8	493	3 Q59846	Q59846 aspergillus
5	1400	50.5	620	3 Q12623	Q12623 humicola gr
6	1394	50.3	579	3 Q12596	Q12596 corticium r
7	1286	46.4	571	3 Q9P4C5	Q9P4C5 lentinula e
8	28.3	609	480	3 Q8J0P8	Q8J0P8 mucor circi
9	728	26.3	579	3 Q7Z7X9	Q7Z7X9 rhizopus or
10	674	24.3	515	3 Q8TFE5	Q8TFE5 baccharomyces
11	187	6.7	599	17 Q96210	Q96210 bullulomyces
12	185.5	6.7	636	17 Q9HLB8	Q9HLB8 thermophilic
13	181	6.5	1588	16 Q8XDG4	Q8XDG4 escherichia
14	174.5	6.3	1236	3 Q9C105	Q9C105 schizosaccharomyces
15	174.5	6.3	659	17 Q97107	Q97107 thermoplasma
16	6.3	990	16	Q83J22	Q83J22 shigella f1

SEARCHED:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPIREMBI_25 : *

1: sp_archea: *

2: sp_bacteria: *

3: sp_fungi: *

4: sp_human: *

5: sp_invertebrate: *

6: sp_mammal: *

7: sp_micr: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: sp_archea: *

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7: sp_micr: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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6: sp_mammal: *

7: sp_micr: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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7: sp_micr: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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6: sp_mammal: *

7: sp_micr: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

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Maximum Match 100%

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6: sp_mammal: *

7: sp_micr: *

8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

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9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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1: sp_archea: *

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8: sp_organelle: *

9: sp_phage: *

10: sp_plant: *

11: sp Rodent: *

12: sp_virus: *

13: sp_vertebrate: *

14: sp_unclassified: *

15: sp_virus: *

16: sp_bacteriap: *

17: sp_archeap: *

Searched:

1017041 seqs, 315518202 residues

<p

DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008938; Glyco_trans_6hp.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00736; GLYHYDRASE15.
 DR PIRSF; PIRSF001031; Glu-a-glcSD_SBD; 1.
 DR SEQUENCE; 639 AA; 68308 MW; 025AD856B6542B69 CRC64;
 Query Match 96.3%; Score 2659.5; DB 3; Length 639;
 Best Local Similarity 98.1%; Pred. No. 3.90-162; Mismatches 6; Indels 3; Gaps 3;
 Matches 521; Conservative 1; Mismatches 6; Indels 3; Gaps 3;
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00820; GLUCOAMYLASE; 1.
 DR PIRSF; PIRSF001031; Glu-a-glcSD_SBD; 1.
 DR Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 PT CHAIN 25 639 GLUCOAMYLASE.
 SQ SEQUENCE 639 AA; 68277 MW; 6F93D0637D174ACB CRC64;
 QY 1 MSFRSLALSGLVCTGLANVISRATDSLWSNEATVARTAILNNIGADGAWNSGADSI 60
 Db 1 MSFRSLALSGLVCTGLANVISRATDSLWSNEATVARTAILNNIGADGAWNSGADSI 60
 QY 61 VVASPSTNDPYFTWTRDSGLVLUKTLVLFRNGDTSLSLTTENYISQAIVQGISNSG 120
 Db 61 VVASPSTNDPYFTWTRDSGLVLUKTLVLFRNGDTSLSLTTENYISQAIVQGISNSG 120
 121 DLSGGAGLGEPKENDEAYTGSGRPQDGPALRATAMIGFGQWLNGYSTATDVW 180
 Qy 121 DLSGGAGLGEPKENDEAYTGSGRPQDGPALRATAMIGFGQWLNGYSTATDVW 180
 121 DLSGGAGLGEPKENDEAYTGSGRPQDGPALRATAMIGFGQWLNGYSTATDVW 180
 181 PLVRNDLSTVAQYMMQTGDUWEEVNGSSPFITAVQHRAVEVEGSAFATAVGSSCSWCDSQ 240
 Db 181 PLVRNDLSTVAQYMMQTGDUWEEVNGSSPFITAVQHRAVEVEGSAFATAVGSSCSWCDSQ 240
 QY 241 APETILCYLOSFWTCSFFILANFDSSRSKGKANT-LIGSINTFPDRAACDSTSOPCSPRAL 299
 Db 241 APETILCYLOSFWTCSFFILANFDSSRSKGKANT-LIGSINTFPDRAACDSTSOPCSPRAL 299
 300 ANHKEVWDPSRFRTYLTINDGSDSEAVAVGRYPEPTYTYNCNPWFCLTAAEQLYDALYOW 359
 Db 300 ANHKEVWDPSRFRTYLTINDGSDSEAVAVGRYPEPTYTYNCNPWFCLTAAEQLYDALYOW 359
 QY 360 DKQGSLEVTDSLDPFKALYSAMGTSSSSTISIVDAVKTFADGVSIVETHASN 419
 Db 360 DKQGSLEVTDSLDPFKALYSAMGTSSSSTISIVDAVKTFADGVSIVETHASN 419
 QY 420 GSMSBQYDKSDGEOLSDARDLWTSYALLTANNRNSVVASWGTTSASSVPGTCATSAI 479
 Db 420 GSMSBQYDKSDGEOLSDARDLWTSYALLTANNRNSVVASWGTTSASSVPGTCATSAI 479
 419 GSMSBQYDKSDGEOLSDARDLWTSYALLTANNRNSVVASWGTTSASSVPGTCATSAI 478
 QY 480 GTTSSVTWPSVTATGGTTTATPTGGSVTSKTTATASKTTTRS 530
 Db 480 GTTSSVTWPSVTATGGTTTATPTGGSVTSKTTATASKTTTRS 530
 479 GTTSSVTWPSVTATGGTTTATPTGGSVTSKTTATASKTTSS 529
 RESULT 2
 Q12537 PRELIMINARY; PRT; 639 AA.
 AC DT 01-NOV-1996 (TREMBrel. 01, Created)
 AC DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 AC DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 AC DE Glucosaminylase precursor (EC 3.2.1.3).
 AC GN GLA.
 AC OS Aspergillus awamori.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OC NCBI_TaxID=110531;
 RN [1] SEQUENCE FROM N.A.
 RP STRAIN=X-100;
 RA Diagne I., Pechexonov V.T., Bulat S.A., Firsov L.M.;
 RT "A glucosaminylase gene from Aspergillus awamori X-100: structure,
 allocation, and gene phylogeny.";
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR US9303; AAB02927.1; -.
 DR HS2P; P0464; 1GAT.
 GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO:0016798; F:hydrolase activity, acting on glycosyl bonds; IEA.
 DR PRINTS; PR00686; CBM_20; 1.
 DR InterPro; IPR002444; CBD_4.
 DR InterPro; IPR002448; EF-hand.
 DR PIRSF; PIRSF001031; Glu-a-glcSD_SBD; 1.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008938; Glyco_trans_6hp.
 DR Pfam; PF00686; CBM_20; 1.
 DR PRINTS; PR00736; GLYHYDRASE15.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00820; GLUCOAMYLASE; 1.
 DR PIRSF; PIRSF001031; Glu-a-glcSD_SBD; 1.
 DR Glycosidase; Hydrolase; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 PT CHAIN 25 639 GLUCOAMYLASE.
 SQ SEQUENCE 639 AA; 68277 MW; 6F93D0637D174ACB CRC64;
 QY 1 MSFRSLALSGLVCTGLANVISRATDSLWSNEATVARTAILNNIGADGAWNSGADSI 60
 Db 1 MSFRSLALSGLVCTGLANVISRATDSLWSNEATVARTAILNNIGADGAWNSGADSI 60
 QY 61 VVASPSTNDPYFTWTRDSGLVLUKTLVLFRNGDTSLSLTTENYISQAIVQGISNSG 120
 Db 61 VVASPSTNDPYFTWTRDSGLVLUKTLVLFRNGDTSLSLTTENYISQAIVQGISNSG 120
 121 DLSGGAGLGEPKENDEAYTGSGRPQDGPALRATAMIGFGQWLNGYSTATDVW 180
 Qy 121 DLSGGAGLGEPKENDEAYTGSGRPQDGPALRATAMIGFGQWLNGYSTATDVW 180
 121 DLSGGAGLGEPKENDEAYTGSGRPQDGPALRATAMIGFGQWLNGYSTATDVW 180
 181 PLVRNDLSTVAQYMMQTGDUWEEVNGSSPFITAVQHRAVEVEGSAFATAVGSSCSWCDSQ 240
 Db 181 PLVRNDLSTVAQYMMQTGDUWEEVNGSSPFITAVQHRAVEVEGSAFATAVGSSCSWCDSQ 240
 QY 241 APETILCYLOSFWTCSFFILANFDSSRSKGKANT-LIGSINTFPDRAACDSTSOPCSPRAL 299
 Db 241 APETILCYLOSFWTCSFFILANFDSSRSKGKANT-LIGSINTFPDRAACDSTSOPCSPRAL 299
 300 ANHKEVWDPSRFRTYLTINDGSDSEAVAVGRYPEPTYTYNCNPWFCLTAAEQLYDALYOW 359
 Db 300 ANHKEVWDPSRFRTYLTINDGSDSEAVAVGRYPEPTYTYNCNPWFCLTAAEQLYDALYOW 359
 QY 360 DKQGSLEVTDSLDPFKALYSAMGTSSSSTISIVDAVKTFADGVSIVETHASN 419
 Db 360 DKQGSLEVTDSLDPFKALYSAMGTSSSSTISIVDAVKTFADGVSIVETHASN 419
 QY 420 GSMSBQYDKSDGEOLSDARDLWTSYALLTANNRNSVVASWGTTSASSVPGTCATSAI 479
 Db 420 GSMSBQYDKSDGEOLSDARDLWTSYALLTANNRNSVVASWGTTSASSVPGTCATSAI 479
 419 GSMSBQYDKSDGEOLSDARDLWTSYALLTANNRNSVVASWGTTSASSVPGTCATSAI 478
 QY 480 GTTSSVTWPSVTATGGTTTATPTGGSVTSKTTATASKTTTRS 530
 Db 480 GTTSSVTWPSVTATGGTTTATPTGGSVTSKTTATASKTTTRS 530
 479 GTTSSVTWPSVTATGGTTTATPTGGSVTSKTTATASKTTSS 529
 RESULT 3
 Q9C1V4 PRELIMINARY; PRT; 618 AA.
 AC Q9C1V4; 416
 DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
 DB Glucosaminylase precursor (EC 3.2.1.3).
 GN GLA.
 OS Talaromyces emersonii.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Talaromyces.

OX NCBI_TaxID=68825;
RN [1]
SEQUENCE FROM N.A.
RA Nielsen B.R., Lehmbbeck J., Frandsen T.P.;
RT "Cloning, heterologous expression, and enzymatic characterization of a
thermostable glucosidase from *Talaromyces emersonii*";
RL Submitted (DEC-2000) to the EMBL/Genbank/DDBJ databases.
DR EMBL; AJ314803; CAC28076.1; --.
DR HSSP; P0464; ICA1.
GO; GO:001339; F:glucan 1,4-alpha-glucosidase activity; IEA.
GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO:0016796; P:polysaccharide metabolism; IEA.
DR InterPro; IPR002044; CBD_4.
DR InterPro; IPR008291; Gluta-a-glcid_SBD.
DR InterPro; IPR00165; Glyco_hydro_15.
DR InterPro; IPR08928; Glyco_trans_6hp.
PFam; PF00686; CBM_20_1.
DR PFam; PF00723; GLYC_20_1.
DR PRINTS; PRO0736; GLYDRLASE15.
DR ProDom; P0001568; CBD_4; 1.
DR PIRSF; PIR00031; Glu-a-glcid_SBD; 1.
KW Glycosidase; Hydrolase; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 28 618 GLUCOAMYLASE.
SQ SEQUENCE 618 AA; 65429 MW; C48A034A2C06E5B2 CRC64;
Query Match 61.0%; Score 1689; DB 3; Length 618;
Best Local Similarity 61.2%; Pred. No. 1.4e-90;
Matches 322; Conservative 75; Mismatches 111; Indels 18; Gaps 5;
QY 7 LALSGLUVCTGLANV-1SKRAT--LDSWLSNEAVARTAILNNIGADGAWGAGDSIVWA 63
9 LCLGLGLPAAFARAPVARAATGSDLSPLATEPIALOGVNLNIGPNAGDVAGASAGIVWA 68
QY 64 PSTNDNDPYFYWTRDPSGLVLKVLDFRNPGTSLISTENIYISAOIVQDSINSPNGDLS 123
69 SPSRSRDPNYYFSWTRDAAITALAKYLVDAFIAGNSKDLCTIQYISAOQKVQTSINPSGDLIS 128
Db 124 SGAGLGRPKFENYDETAATGSGRQPQDGPARATAMMGFGCWLDDNGYTSTADTIVMPV 183
129 TG-GLCGPBKFNNTAETGPNGRPQDGPAKLATAAYANLYLIDGEASTADEIIWPIV 187
QY 184 RNDLSVYAQYMQNTGQDLMEEUNGSSPFTIAVORHALVEAGSAPATAVGSSCSWCDQAPE 243
188 QNDLSVYITQVNSNSTEDLWEVEGGSPFTTAVORHALVEAGNALTRNLHTCSVCQAO 247
Db 244 ILCYQOSFWTQSFLNANF-DASRGKDANTLGSIHTFPDPAACDDSTFQPCSPRALAH 302
248 VLCFLQSYWTSVSYVILANGGGSGRSKGDKVNSTLGSIHTFPDPAAGCCDSDTFQPCSRALAH 307
QY 303 KEWDPSPRSIYTLDGLSDSEAVAVERYPEDTYYNQNPWFCTLAQEQQLDALQWDKO 362
Db 308 KVVTDSFPRSIYAINSGIAEGSAGAVAVGRYPELVDYQGGNPWYIATAAAABQLYDAIKWKKI 367
QY 363 GSLEVTDVSLPPFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGVSIYETHAASNGSM 422
368 GSISITDVSLLPFDQDTPVSAVAGTVNQGSTFENDIISAVQYGDGLSIVKYKTDGSL 427
Db 423 SEQYDKSDGEQSLSARDITWSAALLTANNRNSVVPASWGETSASSVPGTCAATSALGY 482
428 TEQPSRSDTGTIPUSASALTWSIASLUTSARROSVVFPASWGEASSSUPAVCOSATSATGPY 487
QY 483 SVTVTWSWPSTVATGGTTT-TPTGGSVTSKTPATASPKSTT 528
Db 488 STATNTWVPS-----SGSCSSTT'SAPCTTPTPSVAVT 520
RESULT 4 PRELIMINARY; PRT; 493 AA.
ID 059846
AC 059846;
DT 01-AUG-1998 (T-EMBLrel. 07, Created)
DT 01-AUG-1998 (T-EMBLrel. 07, Last sequence update)

01-OCT-2003 (T-EMBLrel. 25, last annotation update)
DT 01-Oct-2003 (T-EMBLrel. 25, last annotation update)
DE Glucosidase.
OS Aspergillus oryzae.
OC Eurotiomycetes; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Aspergillales; Aspergillus.
OK NCBI_TaxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=O-013;
RR MEDLINE=98172744; PubMed=9511753;
RA Hata Y., Ishida H., Ichikawa E., Kawato A., Sugiyama K., Inayasu S.;
RT "Nucleotide sequence of an alternative glucosidase-encoding gene
(RGLB) expressed in solid-state culture of *Aspergillus oryzae*.";
RL Gene 207:127-134(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=O-1013;
RC STRAIN=O-1013;
RA Hata Y., Ishida H., Kojima Y., Ishikawa E., Kawato A., Sugiyama K.,
RA Inayasu S.;
RT "Comparison of two glucosidases produced by *Aspergillus oryzae* in
RT solid-state (koji) and in submerged culture.";
RL Ferment. Biotech. 84:52-53(1997).
EMBL; AB007825; BAM25205.1; --.
DR PIR; PC00723; JG6538.
DR PROSITE; PS00820; GLYCOAMYLASE; 1.
DR PRINTS; PRO0736; GLYDRLASE15.
SQ SEQUENCE 493 AA; 52401 MW; 3707B3A6F0C66256 CRC64;
Query Match 54.8%; Score 1518; DB 3; Length 493;
Best Local Similarity 57.5%; Pred. No. 8.6e-89;
Matches 280; Conservative 82; Mismatches 123; Indels 2; Gaps 2;
QY 5 SIALSGLUVCTGLANVSKRATDSLMSNEAVARTAILNNIGADGAWGAGDSIVWA 64
8 SINATAGAVAHPSFRPKHRSQDNLAFTEACTPIQOGVNLNIGADGCKLVEGAAGIVWA 67
Db 65 PSTNDNDPYFYWTRDPSGLVLKVLDFRNPGTSLISTENIYISAOIVQDSINSPNGDLS 124
68 PSKSNDPYFYWTRDAGLTMEVIRQFFGQDATLSTIQYVDSQANEQAVSNPQGGLSD 127
Db 125 GAGLGRPKFENYDETAATGSGRQPQDGPAKLATAAYANLYLIDGEASTADEIIWPIV 184
128 GSGLAEFRKFYINISQDTSKWRPQDGPAKLASALIAYGNGLISSDKQSVKANIWPIVQ 187
QY 185 NDLSVYAQYMQNTGQDLMEEUNGSSPFTIAVORHALVEAGSAPATAVGSSCSWCDQAPEI 244
188 NDLSVYQYMQNTGQDLMEEUNGSSPFTTAVORHALVEVGSSPFTTAVORHALVEAGDAFAKALGEBCQAC-SVAPQI 246
Db 245 ILCYQOSFWTGSFILANFDSS-RSGKDANTLGSIHTFPDPAACDDSTFQPCSPRALAH 303
247 LCHLQDFWNGSAVLSPNTPNGRSQGDNTNSLGSIHTFPDPAACDDTFFQPCSSRALSNHK 306
QY 304 EVUDSPRSIYTLDGLSDSEAVAVERYPEDTYYNQNPWFCTLAQEQQLDALQWDKO 363
307 LVVDSFRSVIGINNRRGAKAAGVGPYAEIYQGGNPWYIITLTVBELLIDALQWDKO 366
QY 364 SLEVTDVSLPPFKALYSDAATGTYSSSSSTYSSIVDAVKTFADGVSIYETHAASNGSM 423
Db 367 QVNVTTSLPFPFKDLSSNVNTGYSVAKSSAVESLTSVAKYADGFTSVVQBYTPGCGALA 426
QY 424 EQYDKSDGEQSLSARDITWSAALLTANNRNSVVPASWGETSASSVPGTCAATSALGY 483
Db 427 EQYDSRQGTPVSAIDLWTSAAPLAVGRENTPVAFWSNSAVAVPSQCGSGTVGSY 486
QY 484 SVTVTWSW 490
Db 487 TPTVGSM 493

RESULT 5				
Q12623	PRELIMINARY;	PRT;	620 AA.	
ID Q12623				
AC 012623				
DT 01-NOV-1996 (TREMBrel. 01, Created)				
DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)				
DE Glucoamylase (EC 3.2.1.3.)				
GN GLA1.				
OS Humicola grisea var. thermoidea.				
OC Fungi; Ascomycota; mitosporic Ascomycota; Humicola.				
OX NCBI_TaxID=5528;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA Becka R.M., Rey M.W., Thompson S.A., Gray G.L., Carmona C.L.,				
Power S.D.;	"Molecular cloning, analysis and expression of the glal gene encoding a thermostable, raw starch-digesting glucoamylase from the fungus Humicola grisea var. thermoidea."			
RT Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.				
DR EMBL; M69475; AAA33861; -.				
DR HSSP; P04064; IGAT.				
DR GO; GO:0004339; F-glucan 1,4-alpha-glucosidase activity; acting on glycosyl bonds; IEA.				
DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.				
DR InterPro; IPR002044; CBD_4.				
DR InterPro; IPR008231; Glu-a-glcSD_SBD.				
DR InterPro; IPR00165; Glu-a_glyco_15.				
DR InterPro; IPR00828; Glyco_trans_6hp.				
DR Pfam; PF00686; CBD_20; 1.				
DR PRINTS; PR00736; GLYHYDRASE15.				
DR PRODOM; PD01568; CBD_4; 1.				
DR PROSITE; PS00820; GLUCOMYLASE; 1.				
DR PINSF; PIRSF001031; Glu-a-glcSD_SBD; 1.				
DR Glycosidase; Hydrolase.				
DR KW SEQUENCE 620 AA; 66525 MW; 54214FF67E20B0E0A CRC64;				
DR SQ Matches 269; Conservative 96; Mismatches 146; Indels 32; Gaps 7; Best Local Similarity 49.5%; Pred. No. 4e-81;				
Query Match 50.5%; Score 1400; DB 3; Length 620; Best Local Similarity 49.5%; Pred. No. 4e-81; Mismatches 146; Indels 32; Gaps 7; Matches 269; Conservative 96; Mismatches 146; Indels 32; Gaps 7; Best Local Similarity 49.5%; Pred. No. 4e-81;				
DR Y 2 SFRSILALSGIVCTRL----ANVIKTRATLDSWSNEATVARTAILNNIGADGAWVSGA 56				
DR Db 3 TFSKULVLGVSAVQSAQSLGRPHGPISSRLQERAADVTFINTERPIAKWKLNLANIGPNKAQPA 62				
DR Y 57 DSGIVWASPDSTDNPDPYFYWTDRSGIVLKTVLD-LFRNGDTSLSIYSTIENYISAQAVQGI 115				
DR Db 63 AGAVVIAVSFSRTRDPYFPYFTWMPDAALVLTGTEISLGHNTNTL-----QV 108				
DR Y 116 SNPSGDLSSGGGLGPBKPFKNVDTAYTGSNMRQPGPALRATAMIGFGQMLLDNGYTA 175				
DR Db 109 SNPSGTFAOGSGLGSEAKENFLDTAFTGEWGRPQDRGPPRLATAIJOYAKWLIANGYKTA 168				
DR Y 176 TDIVPLVRNLDLSYXVAQYMQNQTGYDYLWEEVNGSSFTIAVQHRAVEGASAFTAVGSSC 235				
DR Db 169 KSVWMPVVKNDLAVIAQYNETEGFDLWEWEPGSSFTIASRHALTEGAYLAQDTECP 228				
DR Y 236 WCDSDAPETLICYLOSPWT--GSPFLANPDS--RSKDANTLGSIHTDPPEAACDDSTP 291				
DR Db 229 PCTTVAPOQLCFOQAFWNNSKGNYVVSTAGTGYSSSSSTYSIVDAVKTFAFDGVSI 288				
DR Y 292 QPCSPRALANKHEVUDSFRSITYLTLGLSDSEAVAVGRPDTTYNGNWFELCLAAEQ 351				
DR Db 289 QPCSPRALANKHEVUDSFRSITYLTLGLSDSEAVAVGRPDTTYNGNWFELCLAAEQ 348				
DR Y 352 LYDALYQWDKGSKGSLEVTDSLDFFKLYSDATGTYSSSSSTYSIVDAVKTFAFDGVSI 411				
DR Db 349 LYDAYUWNKGSGSIVTIVSPLPFRLVSSVSTGYSKSSFTFVINNAVAKYADGFIW 408				
DR Y 412 VETHAASNMSMSEQYDKSDGEQLSARDLTVSYAALLTANNRRNSVTPASW-GETSASSVP 470				
RESULT 6				
Q12596	PRELIMINARY;	PRT;	579 AA.	
ID Q12596				
AC 012596;				
DT 01-NOV-1996 (TREMBrel. 01, Created)				
DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)				
DE Glucoamylase G2 (EC 3.2.1.3.).				
OS				
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes; Aphyliophorales; Corticiaceae; Corticium.				
OX NCBI_TaxID=59291;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=ATH9627;				
RX MEDLINE-96158471; PubMed=8597548;				
RA Nagasaka Y., Muraki N., Kimura A., Suto M., Yokota A.; Tomita F.;				
RT "Cloning of Corticium rolfsii glucoamylase cDNA and its expression in Saccharomyces cerevisiae."; Appl. Microbiol. Biotechnol. 44:451-458 (1995).				
DR EMBL; Da9448; BAM08436.1; -.				
DR HSSP; P04064; IGAT.				
DR GO; GO:0004339; F-glucan 1,4-alpha-glucosidase activity; acting on glycosyl bonds; IEA.				
DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.				
DR InterPro; IPR002044; CBD_4.				
DR InterPro; IPR008231; Glu-a_glcSD_SBD.				
DR InterPro; IPR00165; Glyco_trans_6hp.				
DR InterPro; IPR00828; Glyco_trans_6hp.				
DR Pfam; PF00686; CBD_20; 1.				
DR PRINTS; PR00733; GLYHYDRASE15.				
DR PRODOM; PD01568; CBD_4; 1.				
DR PINSF; PIRSF001031; Glu-a-glcSD_SBD; 1.				
DR Glycosidase; Hydrolase.				
DR KW SEQUENCE 579 AA; 61548 MW; FF56D03F9D1A9EC9 CRC64;				
DR SQ Matches 294; Conservative 77; Mismatches 151; Indels 52; Gaps 11; Best Local Similarity 51.2%; Pred. No. 8.e-81;				
Query Match 50.3%; Score 1394; DB 3; Length 579; Best Local Similarity 51.2%; Pred. No. 8.e-81; Mismatches 151; Indels 52; Gaps 11; Matches 294; Conservative 77; Mismatches 151; Indels 52; Gaps 11; Best Local Similarity 51.2%; Pred. No. 8.e-81;				
DR Y 3 FRSLALALSGIVCTGLANVTKRATLDSWSNEATVARTAILNNIGADGAWVSGADGIVV 62				
DR Db 2 FRSLALAL---ACAVASYSAQSASATAVLTKESAVAKNLGNGQCMSEGAVSGAVI 58				
DR Y 63 ASPSTDNPDPYFYWTDRSGIVLKTVLD-LFRNGDTSLSIYSTIENYISAQAVQGI 121				
DR Db 63 ASPSTDNPDPYFYWTDRSGIVLKTVLD-LFRNGDTSLSIYSTIENYISAQAVQGI 121				
DR Y 178 LIKUDLQYDQVNSDNQTTEDLWEEDDSSFTAVOHRLVQGAFTLQGOTSSASTVSA 237				
DR Y 119 VSTG--GLGEPKFNDTAAFTGANGRPODRGPPRLATAIYTLYNNNGTSVNTLWP 177				
DR Y 182 LVRNDLSSYXVAQYMQNQTGYDYLWEEVNGSSFTIAVQHRAVEGASAFTAVG--SSCSWDS 239				
DR Y 240 QASPLCYQSFN-TGSGTIANFDSSRGDKDANTLGSIHTDPPEAACDDSTFOPCSRA 298				
DR Y 238 TAPSILCFQSYMTNGKWTANTGGGRSGDKDANTLISIHFDSAQSAGSAATSPQCSVA 297				

Qy	299 LANKEKVEDSFRSITYLTNDGLSDSEAVAVGRYFEDTYKINGNPWFCTLAEEQDLYALIQ 358	Db	193 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 252
Db	298 LANIKVYVDSFRSITYLTNDGLSDSEAVAVGRYFEDTYKINGNPWFCTLAEEQDLYALIQ 357	Db	192 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 251
Qy	359 WDKOGSLEVDLSDFKKALYSDAATGTRSSSSSTYSSIVIDAVKTFADGFVSTVTHAS 418	Db	191 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 250
Db	358 WKAAGELNTVSILAFFQOQDSITAGTYTASSSVYTLISDIOQAFAEFDVIAKTPS 417	Db	190 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 249
Qy	419 NGMSSEQYDKSDERGQSLARDLTVSYAALTANRNSUPASGETSASSVPCTA--AT 476	Db	189 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 248
Db	418 SGFLSEQYDKSTGQDQAANLTWSYAAAITAYQARNGFTGASWG---AKGVSTSCSGAT 474	Db	188 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 247
Qy	477 SAIGTYYSSVT-----SWISIVATG----GTTTAT-----PTCGGSVIST 514	Db	187 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 246
Db	475 SPGGSGSDEVTDVYATVYQGNIYTGDSVSLGNWPANGVALSSANYPTWSATIALP 534	Db	186 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 245
Qy	515 SKTT-----ATASKSTTTRG 531	Db	185 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 244
Db	535 ADTTIQKYVNIDGGSNTVWBDAISNREITTPASG 568	Db	184 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 243
RESULT 7			
Qy	OP94C5 PRELIMINARY; PRT; 571 AA.	Db	183 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 242
AC	OP94C5; 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	Db	182 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 241
DT	01-OCT-2000 (TREMBLrel. 25, Last annotation update)	Db	181 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 240
RP	SEQUENCE FROM N.A.	Db	180 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 239
RX	MEDLINE=2,092826; PubMed=10831434;	Db	179 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 238
RA	ZHAO J., Chen Y.H., Kwan H.S.; "Molecular Cloning, Characterization, and Differential Expression of a Glucosamylase Gene from the Basidiomycetous Fungus <i>Lentinula edodes</i> .", Appl. Environ. Microbiol. 66:2531-2535 (2000).	Db	178 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 237
DR	EMLBL; P0420541; AAFT5523; 1. --.	Db	177 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 236
DR	HSSP; P04064; 1GA1.	Db	176 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 235
DR	GO; GO:0003924; F:catlytic activity; IEA.	Db	175 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 234
OC	Agaricales; Tricholomataceae; Lentiniula.	Db	174 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 233
NCBI_TaxID	5353;	Db	173 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 232
RN	[1]	Db	172 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 231
RESULT 8			
Qy	OBJJOPB PRELIMINARY; PRT; 609 AA.	Db	171 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 230
AC	OBJJOPB; 01-MAR-2003 (TREMBLrel. 23, Last sequence update)	Db	170 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 229
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	Db	169 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 228
DR	Glucosamylase GLAM.	Db	168 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 227
OS	Mucor circinelloides.	Db	167 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 226
OC	Bakteria; Fungi; Zygomycota; Mucorales; Mucoraceae;	Db	166 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 225
OX	Mucor.	Db	165 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 224
NCBI_TaxID	36080;	Db	164 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 223
RN	[1]	Db	163 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 222
RP	SEQUENCE FROM N.A.	Db	162 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 221
RA	Houghton-Larsen J., Pedersen P.A.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.	Db	161 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 220
RL	DR EMBL; AY163303; ANN8206.1. --.	Db	160 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 219
DR	InterPro; IPR002044; CBD4.	Db	159 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 218
DR	InterPro; IPR008291; Glu-a-glcstd SBD.	Db	158 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 217
DR	InterPro; IPR00165; Glyco_hydro_15.	Db	157 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 216
DR	InterPro; IPR00828; Glyco_trans_6hp.	Db	156 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 215
DR	Pfam; PF00586; CBM 20; 1.	Db	155 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 214
DR	PF00723; Glyco_hydro 15; 1.	Db	154 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 213
DR	PRINTS; PR00736; GLYHYDRLASE15.	Db	153 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 212
DR	Prodrom; PDB01568; CBD 4; 1.	Db	152 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 211
DR	PROSITE; PIRSP001031; Glu-a-glcstd SBD; 1.	Db	151 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 210
DR	SEQUENCE 571 AA; 6161 MW; AIBDIBCC84E97FF CRC64;	Db	150 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 209
Qy	Query Match 46.4%; Score 1286; DB 3; Length 571; Best Local Similarity 47.9%; Pred. No. 6.7e-74; Matches 266; Conservative 91; Mismatches 150; Indels 48; Gaps 10;	Db	149 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 208
Qy	19 NVTSKRATLDSWISNEATVARTAILNNTGADGAWVGSGADSGTIVASISTNDNFDFYWTWTR 78	Db	148 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 207
Db	14 SWAQSSVTLDFLRNG-DTSLSLTIENNTSADQIVQGINSNPGCDLSGAGLGKPKENFE 137	Db	147 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 206
Qy	74 DSGLVLTQIDTQGFTDTRIBNDVGAQIVQPNPSDITTG-GLGPKPENFE 132	Db	146 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 205
Db	138 TAVGSGWRPQRDGPAALRATAMIGFGQMLNDGYTSTATDIVPLVNLDSVAQYQNMOTGD 197	Db	145 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 204
Qy	133 TAFIGPWRPQRDGPAALRSTALTWANTLISBGNTFYVTDLPIENDLNTVSSNNQS 192	Db	144 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 203
Qy	198 GYLWLEEWNGSSFTTIAVQHRAVLVEGSAFATAVG--SSCSWCDSQAPBILC1QSFN--T 253	Db	143 TDLWEEIYSSFFSTAVORHLRQGTTLGRAIGQNLASSYGNQADFLCLTQLSYNPT 202

Db 342 LWEEEVNGVHRYTLMRRLGKFGANFATRNGDSTRATTNTAASKTKIDSFRNSNGQY 401
 QY 257 I-LANFD---S-SRGKDANTL---LGS-IHTPDEAACDSTTOPCS-PRALAHKEVUDS 308
 Db 402 VSVSQS-VTCGVSKAGYDASVLAISNLGS- 452
 QY 309 PRSIYTLDGLSDSEBAVGRYPEDTY---YNGNPWFLCTLAEEQLYDLYQWDKQG 363
 Db 453 PASLYSINQNLNGVIGNAIGRYPEDTYNGNGSQGNPWFICNAEFLYRAKEWPFN 512
 QY 364 SLEYTDVSDLPFKALYSIATGT-YSSSS-TYSSIVDAYKTFADGFVSI-VEFHASNISM 422
 Db 513 GVTYVTSISLNFFKKFDSSAAGVGTKVGTGFSNLSLVQNVAVAADFSTIKFHATNGSM 572
 QY 423 SEQYDKSDGEQLSARDLTMVYALLTAN 450
 Db 573 SEQYGRADGCLMTGARDLTWSHASLISAS 600

RESULT 9

ID Q727X9 PRELIMINARY; PRT; 579 AA.
 AC Q727X9; Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Glucoamylase (Fragment).
 OS Rhizopus oryzae (Rhizopus delemar).
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC Rhizopus.
 RN NCBI_TAXID=64495;
 RP SEQUENCE FROM N.A.
 RA Chen G., Yu X.C., Jiang H.Z., Li M.G.; Submitted (ANG-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AV359821; AAQ18643.1; -.
 FT NON_TER 1
 FT CHAIN <1
 FT CHAIN 27
 FT CHAIN 86
 SQ SEQUENCE 579 AA; 62.51 MW; 75811D9336BBB8751 CRC64;

Query Match 26.3%; Score 728; DB 3; Length 579;
 Best Local Similarity 37.1%; Pred. No. 2.8e-38;
 Matches 166; Conservative 70; Mismatches 170; Indels 42; Gaps 10;

QY 25 ATLDWSLWSNEATVARTAILNNITGADGAWVSGADSGIVVASPSTONPDYFTWTRDSGLVL 84
 Db 143 STISSWIKKQOBEGISRFAMLRNINP---PGSATOFIAASLISTAGPDYYTAWTRDALIS 197
 QY 85 KTLDFLFR--NGDTSLISTENYSAOIAVQOGISNPSGDLLSSGAGLGPKENDETAV 141
 Db 198 NVIVEYNTTISLGNKNTILVNLKDVTFSVKQTSTVCN---CLGEPKENDGSGT 251
 QY 142 GSWRGPQRDPALRATAMIGFFQ-WLDDNGYTSSTATIDWPLVNRDLSYVAQYMQNTGYD 200
 Db 252 GAWGRP-RONPQAERATTFILFADGTYLTOKDAVYTGTLKPAIFKDQDVWNWNSCUD 311
 QY 201 LWEEEVNGSFTTIAVQHRALEVGSAFATAVGSS---CSWCDSQABEILCILQSFWMSFIL 258
 Db 312 LWEEEVNGVHRYTLMRRLGKFGANFATRNGDSTRATTNTAASKTKIDSFRNSNGQY 371
 QY 259 ANFDS---SRSKDANTL---LGS-IHTPDEAACDSTTOPCS-PRALAHKEVUDS 308
 Db 372 IQVSQSVTGGVSKKGCLDVSTLAANLGSV---DGGFTPGSEKILATAVEDS 422
 QY 309 FIRSTYLNDGLSDSEAVGRYPEDTY---YNGNPWFLCTLAEEQLYDLYQWDKQG 363
 Db 423 PASLYSINQNLNGVIGNAIGRYPEDTYNGNGSQGNPWFICNAEFLYRAKEWPFN 482
 QY 364 SLEYTDVSDLPFKALYSIATGT-YSSSS-TYSSIVDAYKTFADGFVSI-VEFHASNISM 422

RESULT 10

ID Q8TPE5 PRELIMINARY; PRT; 515 AA.
 AC Q8TPE5; Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)

DE Glucoamylase precursor (EC 3.2.1.3).
 GN GLU 011.
 OS Saccharomyces fibuligera (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycidae; Saccharomyces;
 OC Saccharomyces; NCF1_TAXID=4944;
 RN {1}
 RP SEQUENCE FROM N.A.
 RC STRAIN=IFO 0111;
 RA Hostinova B., Solovicova A., Janecek S., Gasperik J.;
 RT "Raw starch degrading glucamylase from Saccharomyces fibuligera:
 molecular cloning and expression in yeast.",
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AU311987; CAC83969.1; -
 GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IEA.
 DR GO; GO_0005976; P:polysaccharide metabolism; IIA.
 DR InterPro; IPR00655; Glyco_hydro_15.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR PRINTS; PR0736; GLYDRASE5.
 DR PROSITE; PS00820; GLUCOAMYLASE; 1.
 KW Signal; Hydrolase; Glycosidase.
 FT SIGNAL 1
 FT CHAIN 27
 SQ SEQUENCE 515 AA; 57423 MW; A2P2T79EEA842AE0 CRC64;

Query Match 24.3%; Score 674; DB 3; Length 515;
 Best Local Similarity 33.7%; Pred. No. 6.7e-35;
 Matches 163; Conservative 82; Mismatches 177; Indels 62; Gaps 16;

QY 24 RATLDWSLWSNEATVARTAILNNITGADGAWVSGADSGIVVASPSTONPDYFTWTRDSGLVL 84
 Db 41 RSNTFQWHEQPAVSWYVLYLQNTDYPEGOFPSKAQPGVWAVASPTESEPPIFYQTRDTAIT 100
 QY 64 LKTLVDLFRN--GDTSLISTENYSAOIAVQOGISNPSGDLLSSGAGLGPKENDETAV 138
 Db 101 FLSLIAEVNEDHSFSNTTIAKUVETYVISNTYLOVRNSPGNFSPNPHDQGPKENPVNDT 160
 QY 139 AYTSGWGRQRDGPALRATAMIGE-----GQWL--DNGY-T-STATIDWPLVNRD 186
 Db 161 AYTASWGRQNDGPALRAYSIRVNAVKHNGKLQAGQNPYSSASDITWIKIIPD 220
 QY 187 LSYYAQYMQNTGQYDLEEEVNGSFTTIAVQHRALEVGSAFATAVGSS---CSWCDSQABE 244
 Db 221 LQHSTHWTSGFLWEEQGTHFTIALVQLKALSYGFLPLSKTYNDPGFTSMLKQKAL 280
 QY 245 LCYQSFWFGSEFILANFD-----SSRGKDANTLGS-IHTPDEAACDSTTOPCS-PRALAHKEVUDS 344
 Db 281 NSYINS---SGFVNKGKHIVESPOLSSRGGLSDATY-TALITHD--IGDDDTYTPPN- 333
 QY 297 RALAHKEVUDS-----RSIYTLDGLSDSEAVGRYPEDTY---YNGNPWFLC 344
 Db 334 ---VDSVYVLSVLYLVLVNUKNRKVINGNY--KAGAAGRYPEDVYNGVGTGSGNPWQLA 388
 QY 345 TAAAEQLOLTDYKMD-QCSLEVTDVSDUFFKALYSDA-TCTYSS-----SST 393
 Db 389 TAYAGQFTFTLAMSLNSKNNKLVEKLNDLYNSFIADJSKDSIYSSAKDSLITYGSDN 448

QY 394 YSSIVDAVKTFRDGFSIVSIVEHTHAASNSMSQYDKDGEQISARDLTWSYALITANRR 453
|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 449 VKNVIKSLQRDSFLKVILPHIDNGQNLTHBIRYTGFOAGAVSLTWSSGSSLNAR 508
|::|::|::|::|::|::|::|::|::|:
QY 454 NSVW 457
|::|:
Db 509 NGLI 512
|::|:
RESULT 11
Q96210 PRELIMINARY; PRT; 599 AA.
ID Q96210
AC 096210;
DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein ST2017.
GN ST2017.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus;
OX NCBI_TAXID=11955;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka Y., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagi M., Nishimura M., Yamagishi A.,
RA Ohshima T., Kikuchi H.,
RT "Complete genome sequence of an aerobic thermoacidophilic
Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
EMBL_AP000988; BAB7116_1; -
DR GO; GO:0016020; C:membrane; IBA.
DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IBA.
DR GO; GO:0005215; F:transporter activity; IBA.
DR GO; GO:0005976; P:polysaccharide metabolism; IBA.
DR GO; GO:0006100; P:transport; IBA.
DR InterPro; IPR00165; Glyco_hydro_15.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00723; Glyco_hydro_15_1.
DR PROSITE; PS00430; TonB DEPENDENT_RBC 1; 1.
KW Hypothetical protein; Complete proteome;
SQ SEQUENCE 599 AA; 69661 MW; F8B94CAE7731D119 CRC64;
Query Match 6.7%; Score 187; DB 17; Length 599;
Best Local Similarity 22.3%; Pred. No. 0.001; Matches 102; Conservative 58; Mismatches 151; Indels 146; Gaps 23;
QY 29 SWL---SNEATVAPAIL---NNIGADGAWGAGSDGSIWVASPSTDNPDXYTWR 78
|::|::|::|::|::|::|::|::|::|:
Db 235 AWLVKARDYDPSLVRSLILHAWHORN---GALPAALDTDUMRNDT---YNYVWHR 286
|::|::|::|::|::|::|::|::|::|:
QY 79 DSGVLVLTFLVLRNGDTSLISTENIYISAQAIQVGISINSSGDLSSGAGIGBPKENDET 138
|::|::|::|::|::|::|::|::|::|:
Db 287 DAAF-----ASIALTGY---QDPIRNLNFNTKPLPNGFDFQ-KTCDF-- 327
|::|::|::|::|::|::|::|::|::|:
QY 139 ATYGSWGRP-----QRDGPALRATMIGCOWLIDNGYSTATIDVWPLVRNDL 187
|::|::|::|::|::|::|::|::|::|:
Db 328 ---GNWGSTMWPNPNSPIQED----ETAMLYALWVHRSRFTD-IDFVRPLYAPFV 377
|::|::|::|::|::|::|::|::|::|:
QY 188 SYVAQOWM-----NOTC-----YDLMREVNNSSPFTIAVQHARHALVEGSAFATAVSSCSWC 237
|::|::|::|::|::|::|::|::|::|:
Db 378 KXIAEFLVLSYRDEETGLPLBSYDLMWERLGHTFFSLAVVAGLMSAYKFABPFGBDE-NLK 436
|::|::|::|::|::|::|::|::|::|:
QY 238 D---SQAPEIICYLQOSFWTGS-FILANFDSSRSKG---DANIILGSIHTFDEAACDSTP 291
|::|::|::|::|::|::|::|::|::|:
Db 437 DKLTAANEVEVKGLERFYVGDHFARTIYEDNSIDKTVDASTLFASIL-----GPF 486
|::|::|::|::|::|::|::|::|::|:
RESULT 12
Q9HL88 PRELIMINARY; PRT; 636 AA.
ID Q9HL88
AC 09HL88;
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein Ta0342.
GN TA0342.
OS Thermoplasma acidophilum.
OC Archaea; Buryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TAXID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1778;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
acidophilum.;"
RL Nature 407:503-513(2000).
DR EMBL_AL445064; CACT1486_1; -
DR GO; GO:0004339; F:glucan 1,4-alpha-glucosidase activity; IBA.
DR GO; GO:0005976; P:polysaccharide metabolism; IBA.
DR InterPro; IPR00165; Glyco_hydro_15.
DR InterPro; IPR008928; Glyco_trans_6hp.
DR Pfam; PF00723; Glyco_hydro_15_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 636 AA; 73269 MW; FFA46856CCDE9AFD CRC64;
Query Match 6.7%; Score 185.5; DB 17; Length 636;
Best Local Similarity 19.0%; Pred. No. 0.0014; Matches 86; Conservative 56; Mismatches 139; Indels 171; Gaps 15;
Matches 86; Conservative 56; Mismatches 139; Indels 171; Gaps 15;
QY 57 DSGIVASAPSTD-----NPDXYTWRDSLGVLKTLVUDLFRNGDTS-LISTENIYSAQ 109
|::|::|::|::|::|::|::|::|::|:
Db 281 DLGATASCDSDILKLSHDGYYVWPRDASMAYAL-SISGHSETARRFFPALMEDSSEE 339
|::|::|::|::|::|::|::|::|::|:
QY 110 AIWOGISNPSCDLSGGAGIGBPKENDETAYTGSGWRPDRGPAI---RATAMIGFGQ 164
|::|::|::|::|::|::|::|::|::|:
Db 340 GYLHKYKVNQDKIAS-----SWLPHMVNGKSYIYPQDEDETALVWVAL 381
|::|::|::|::|::|::|::|::|::|:
QY 165 WLDNGYSTSTATIDVWPLVRNDLSTVQAQYMN-----QTYGDLMWE 204
|::|::|::|::|::|::|::|::|::|:
Db 382 WEYFKY-----NDIGTAPYVLERLTRADEFMTNFVDNGNGLPKRPFQDLE 428
|::|::|::|::|::|::|::|::|::|:
QY 205 VNGSSFTIAVQHARHALVEGSAFATAVSSCSWCSDSQAPETICLYQSFWTGCFILANFDSS 264
|::|::|::|::|::|::|::|::|::|:
Db 429 RYGIHAYTVAVVAALKAAKSNFANVFG-----DDP 458
|::|::|::|::|::|::|::|::|::|:
QY 265 RSKDQANTLTGSIHTFDEAACDSTPQCPSPRALANHKE--VVDFSRSIYTLDGLPS 322
|::|::|::|::|::|::|::|::|::|:
Db 459 LSEKVTENAAEMYHADEFPYSEDIGY---ARAIDKGPDFTDVDSLTLVLF-GFMKDA 514
|::|::|::|::|::|::|::|::|::|:
QY 323 E-----AVAVGPRYPEDTYN-----GIPWELCTLAABEOLYDA 355
|::|::|::|::|::|::|::|::|::|:
Db 515 DDPKVISTMORISEDLWVNGVGIIARYQNDYRMVKDDSVPGNPWITLWMA-RYMR 573
|::|::|::|::|::|::|::|::|::|:

Query Match 6.3%; Score 175; DB 3; length 1236;
 Best Local Similarity 21.5%; Pred. No. 0_016;
 Matches 129; Conservative 91; Mismatches 242; Indels 138; Gaps 21;

DR InterPro; IPR008928; Glyco_trans_6hp.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 KW Complete proteome.
 SEQUENCE 659 AA; 76598 MW; 3610F5405F13B33 CRC64;

Query Match 6.3%; Score 174; DB 17; Length 659;
 Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

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'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

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'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

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Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

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'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Query Match 6.3%; Score 174; DB 17; Length 659;

'Best Local Similarity 19.7%; Pred. No. 0.0071; Mismatches 158; Indels 159; Gaps 16;

Matches 90; Conservative 49; Mismatches 158; Indels 159; Gaps 21;

Search completed: June 17, 2004, 17:47:29

Job time : 50 secs

RESULT 15

Q97BM7 PRELIMINARY; PRT; 659 AA.

AC Q97BM7; DT 01-OCT-2001 (TREMBL1, 18, Last sequence update)

DT 01-OCT-2003 (TREMBL1, 25, Last annotation update)

DB Glucosaminylase; TVG041561.

GN Thermoplasma volcanium.

OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;

OX NCBI_TAXID=50339; [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GSS1 / DSM 4299 / JCM 9571;

MEDLINE=00570466; PubMed=111211031;

Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawamoto T.,

Ra Kawashima-Ohyu Y., Watanabe K., Yamazaki M., Kanohori K., Suzuki M.,

Nunohiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,

"Archaeal adaptation to higher temperatures revealed by genomic

sequence of *Thermoplasma volcanium*";

Proc. Natl. Acad. Sci. U.S.A. 97:14267-14262(2000).

EMBL: AP001092; BAB59570.1; -

GO: GO_0004339; F:Glucan 4-alpha-glucosidase activity; IBA.

DR GO_0004339; F:Glucan 4-alpha-glucosidase metabolism; IBA.

DR GO_0005976; P:Polybactin-like metabolism; IBA.

DR InterPro; IPR000165; Glyco_hydro_15.

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OM protein - protein search, using sw model

Run on: June 17, 2004, 17:36:33 ; Search time 18 Seconds
 (without alignments)

1544.748 Million cell updates/sec

Title: US-10-038-723-2

Perfect score: 2771
 Sequence: 1 MSFRSLIALSGLVCTGLANV.....SKTTATASKTSTTRSGMSL 534

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2742	99.0	640	1 AMYG ASPNG
2	2620	94.6	639	1 AMYG ASPSH
3	2588.5	93.4	639	1 AMYG ASPKA
4	1935	69.8	612	1 AMYG ASPOR
5	1577	56.9	626	1 AMYG NEURC
6	1321	47.7	616	1 AMYG HORRE
7	781.5	28.2	450	1 AMYG SCHPO
8	725	26.2	604	1 AMYG RUOR
9	671.5	24.2	519	1 AMYH SACFI
10	664.5	24.0	519	1 AMYH SACFI
11	641.5	23.2	624	1 AMYH ARXAD
12	597	21.5	549	1 AMYH YEAST
13	522	18.8	767	1 AMYH SACDI
14	521	18.8	768	1 AMYI SACDI
15	221.5	8.0	615	1 YGL10_METJU
16	159.5	5.8	1196	1 ICER_PBSX
17	159	5.7	1210	1 ICEN_PSEPL
18	158	5.7	670	1 YEGG_SCHPO
19	158	5.7	3178	1 YSB9_CABEL
20	157	5.7	1258	1 ICEN_EBWHE
21	156.5	5.6	540	1 GKL1_ASPPAC
22	155.5	5.6	1148	1 ICER_PBSX
23	155	5.6	1322	1 ICER_PANAN
24	154.5	5.6	1200	1 ICEN_PEST
25	151.5	5.5	1034	1 ICEN_PANAN
26	151.5	5.5	1306	1 MBB2_YEAST
27	151.5	5.5	1331	1 MABN_CALSA
28	150	5.4	1609	1 FIG2_YEAST
29	147	5.3	507	1 YG46_YEAST
30	142	5.1	1419	1 ALA1_CANAL
31	141.5	5.1	644	1 XND_CELIFI
32	141	5.1	1802	1 HCR1_YEAST
33	140.5	5.1	1567	1 ICEN_XANCT

OC Eukarya; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

RN [1] NCBI_TaxID=5061, 103531;

RP SEQUENCE FROM N.A.

RC SPECIES=A.niger;

RX MEDLINE=84261158; PubMed=6204865;

Boel B., Hansen M.T., Hjort I., Hoegh I., Filil N.P.;

"Two different types of intervening sequences in the glucoamylase gene from Aspergillus niger.",

RN [2]

RX

RC SPECIES=A.niger;

RX

SPECIES=A.niger;

RX

SEQUENCE OF 84236105; PubMed=6203744;

RX

Boel B., Hjort I., Svensson B., Morris F., Norris K.E., Filil N.P.;

RX

"Glucamylases G1 and G2 from Aspergillus niger are synthesized from

RX

two different but closely related mRNAs.",

RX

EMBO J. 3:1097-1102(1984).

RX

[3]

RX

SEQUENCE OF 25-640, AND COMPARISON OF FORMS G1 AND G2.

RX

RX

SPECIES=A.niger;

RX

MEDLINE=86136085; PubMed=3081341;

RX

Svensson B., Larsen K., Gunnarsson A.;

RX

"Characterization of a glucoamylase G2 from Aspergillus niger.",

RX

Bur. J. Biochem. 154:497-502(1986).

RX

[4]

RX

SEQUENCE OF 25-640.

RX

SPECIES=A.niger;

RX

Svensson B., Larsen K., Svensson I., Boel B.;

RX

"The complete amino acid sequence of the glycoprotein, glucoamylase

RX

Gi, from Aspergillus niger.",

RX

Carrisberg Res. Commun. 48:529-544(1983).

RX

[5]

RX

SEQUENCE FROM N.A.

RX

SPECIES=A.awamori;

RX

MEDLINE=8505934; PubMed=644004;

RX

Numberg J.H., Meade J.H., Cole G., Lawyer F.C., McCabe P.,

RX

Schweickart V., Tal R., Wittman V.P., Platgaard J.E., Innis M.A.;

RX

"Molecular cloning and characterization of the glucoamylase gene of

RX

Aspergillus awamori.",

RX

Mol. Cell. Biol. 4:2306-2315(1984).

RX

[6]

RX

REVISIONS.

ALIGNMENTS

34	138.5	5.0	600	1 SP96 DICDI
35	138	5.0	797	1 VGLX HSVEB
36	137	4.9	556	1 WSC3 YEAST
37	136	4.9	542	1 CH12 RHOL
38	136	4.9	995	1 YIQ9 YEAST
39	135.5	4.9	537	1 GU11 PRMIA
40	133.5	4.8	1589	1 PHP_DROME
41	132	4.8	827	1 XANP XANS2
42	130.5	4.7	1537	1 PLO1 YEAST
43	130.5	4.7	1746	1 TENA PIG
44	130	4.7	706	1 PLB2 YEAST
45	129.5	4.7	1367	1 AMYH YEAST

P14328 dictyosteli

P28968 equine herb

Q12215 saccharomy

P29027 rhizopus ol

P40442 saccharomy

Q06886 penicillium

P39769 drosophila

O60106 xanthomonas

P32768 saccharomy

Q29116 sub scrofa

P08640 saccharomy

RA Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J., Schulz U.; in the genome of a filamentous fungus? Analysis of the "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence." RT Neurospora genome sequence. RL Nucleic Acids Res. 31:1944-1954 (2003). RN [3]

RP SEQUENCE OF 36-65.

RC STRAIN=74-OR23-1A / FGSC 987;

RA Koh-Luar S.I., Parish J.H., Bleasby A.J., Pappin D.J.C., Ainley K., Johansen P.E., Radford A.; Exported proteins of Neurospora crassa: 1-glucosamylase. RL Enzyme Microb. Technol. 11:692-695 (1999).

RT -- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.

CC -- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.

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CC

DR EMLU; X67291; CAA47707_1; -;

DR EMBL; AL355932; CAB91426_1; -;

DR HSSEB; PO4064; 1GAT.

DR InterPro; IPR002044; CBD_4.

DR InterPro; IPR008291; Glu-a-glcid_SBD.

DR InterPro; IPR00165; Glyco_hydro_15.

DR InterPro; IPR008928; Glyco_trans_6hp.

DR Pfam; PF00685; CBM_20_1.

DR Pfam; PF00723; Glyco_hydro_15_1.

DR Pfam; PF00131; Glu-a-glcid_SBD; 1.

DR PRINTS; PR00736; GLYDRASE15.

DR PRODOM; PDO001568; CHD_4; 1.

KW Hydrolase; Glycosidase; Polysaccharide degradation; glycoprotein; KW Signal.

FT PROPEP 1 19 POTENTIAL.

FT PROPEP 20 35 POTENTIAL.

FT CHAIN 36 626 GLUCOAMYLASE.

FT BINDING 155 155 SUBSTRATE BY SIMILARITY.

FT ACT_SITE 211 211 CATALYTIC BASE (BY SIMILARITY).

FT ACT_SITE 214 214 GENERAL ACID CATALYST (BY SIMILARITY).

FT ACT_SITE 215 215 INTERACT WITH SUBSTRATE (BY SIMILARITY).

FT CARBOHYD 106 106 N-LINKED (GLCNAC. .) POTENTIAL.

FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 217 217 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CONFLICT 82 82 MISSING (IN REF. 1).

FT CONFLICT 550 550 A -> R (IN REF. 1).

FT CONFLICT 560 560 V -> L (IN REF. 1).

FT CONFLICT 626 AA; 6647 MW; 5458BDDBA7A3B349 CRC64;

SQ SEQUENCE

Query Match 56.9%; Score 1577; DB 1; Length 626; Best Local Similarity 57.6%; Pred. No. 8.6e-97; Matches 306; Conservative 85; Mismatches 130; Indels 10; Gaps 6;

Qy 2 SFRSLAISLGVLCLANVISKRATLDSMSNEATVAPALIANNIGADGAWSGADSGIV 61

Db 13 AFOAVTGLPDPPLHEKRHSIDTISVSDSYQTETPIAQKLNLNIGASCGRASAGTV 71

Qy 62 VASPTDNPDVFYWTDRDSLGLVVKLTKLVDLFRNG-DTSLISTENIVISAQIVQTSNSPG 120

Db 72 VASSKSSPDWYWTDRDAALVTKLVIDEFTNDYNTLQNTIQAYAAQKLQGVSNPG 131

Qy 121 DLSSCAGLCPKFNEDTAYTGSKRPQRDGPALRATAMIGFGWMLDNGYTSATDIW 180

Db 132 SLSNGAGLGPKFMDLQOFTGANGRPORDGPPLKALIGYGRWLSNGYADAKSIW 191

Qy 181 PLVENDLSTVVAQYMQNTGVDLWEENGSSFTIAVORHALVEAGAFATVGSSCSWCDSQ 240

DB 192 PIVENDLAVTAQYMWNTCDLWBEVNSSSFPTIAASHHALVSGSAFKASVGSCSACDAI 251

RP SEQUENCE OF 72-76, AND CHARACTERIZATION.

RC MEDLINE=90338987; PubMed=2116499;

RA Fagerstroem R., Vainio A.E.I., Suoranta K., Pakula T., Kalkkinen N., Torkkeli H.T.; Comparison of two glucosamylases from Hormoconis resinae. RL J. Gen. Microbiol. 136:913-920(1990).

RT -- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.

CC -- SUBCELLULAR LOCATION: Secreted.

CC -- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.

CC

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DR PRINTS; PR00736; GLYHYDRASE5.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
 KW Signal; Meiosib.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 28 BY SIMILARITY.
 FT CHAIN 29 450 PROBABLE GLUCOAMYLASE.
 FT BINDING 147 147 SUBSTRATE (BY SIMILARITY).
 FT ACT_SITE 203 203 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 206 206 GENERAL ACID CATALYST (BY SIMILARITY).
 FT ACT_SITE 207 207 INTERACT WITH SUBSTRATES (BY SIMILARITY).
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 409 409 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 450 AA; 51163 MW; 31C5BF2A8E4785FE CRC64;

Query Match 28.2%; Score 781.5; DB 1; Length 450;
 Best Local Similarity 37.6%; Pred. No. 1.9e-44; Indels 63; Gaps 12;
 Matches 179; Conservative 68; Mismatches 166; Delins 63; Gaps 12;

QY 7 LAISGLIVCTG--LANVIRKATDSWLSNEATARTAATLNNIGADGAWSGADSGIWA 63
 8 LLLGGCVNSABSLSPNPKRSKEASMDWEPOQKGIGAMGHMNNIGDSGM@AKDINGPCIIA 67

QY 64 SPSTNDNPFDYTWDRDSGLVTKTVDLFENGTDTSLSLTENYISQAQAVQGISPNPGDLS 123
 68 SPSTDSPDYYQWYRDSLALTMTLDRFBDKGLEPIVYKMDMVRUQLQKVNPNSGDFY 127

QY 124 SGAGLGEPKENDTAYTGSWGRQFDGALLRATAMIGQFQWILLDNGTSTATIDIVPLV 183
 128 AG-SLGEPKENPDGTSYDGDWGRFQNDSPALARATAFIKYQNNLFENGKEVHEVWIAV 186

QY 184 RNDLSYVAQWQNQGYDLMBVNGSSSFETAVORRALVRESAFAVAVESSSCWSDQAE 243
 187 LADDYTANHWTTEASFDLMEBEKWHIFTLAVQGRAMQDGTAFAKRIG-----APD 237

QY 244 -ILCYLOSF-W-TGSFILAFDS-S-SRGKDANTLGSHT--FDPPEAACD 287

Db 238 QAIHQYRQTTEPIDKJGFEPWDGPMVGVIKGYGRVDRSGLDCSTIASLYSNEFD---- 291

QY 288 DSTROPQCSRALAHKKEVUDPSRSIYTLDGLSSEAVAVGRYPTYN---GNPMP 342
 292 -MHLPLRLKQBTMTRDYPVNQWKGQ---AMGRYPEPDVTDGVSKSIGNPWF 339

Db 343 LCTLAAREQDIAJQWQDGQSLVTDVSLDFK--ALVSDAATGTYSSSSTSIIVA 400
 340 ICITSSAAETIYKAYDNGKLPELTYINHFFMKFAEGD-----PYNWSVIRKN 390

QY 401 VTKTADGFVSIYETHAASNGMSRSQYDKSDGEOLSAIDLTVSYALLTANNRRNSV 456
 391 MHTYADNFLEKAVAFQHNGSMSQFSRUDGHQKGARDLTWYSILLNAYRREAI 446

RESULT 8

AMYG_RHTOR STANDARD; PRT; 604 AA.

AC P07683; DT 01-APR-1988 (Rel. 07, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-May-2000 (Rel. 39, Last annotation update)
 DE Glucoamylase precursor (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase)
 DE (1,4-alpha-D-glucan glucohydrolase).
 OS Rhizopus oryzae (Rhizopus *dilemati*).
 OC Rhizopus; Fungi; Zygomycota; Zygomycetes; Mucorales; Mucoraceae;
 OC NCBI_TaxID=64495;
 RN [1] R.P. SEQUENCE FROM N.A.
 RC STRAINSAM0034;
 RA Asikari T., Nakamura N., Tanaka Y., Kiuchi N., Shibano Y.,
 RA Tanaka T., Amachi T., Yoshiumi H.,
 RT Rhizopus raw-starch-degrading glucoamylase: its cloning and
 RT expression in yeast.;
 RL Agric. Biol. Chem. 50:957-964 (1986).

QY 25 ATUDSWLNNEATARTAATLNNIGADGAWSGADSGIWA[PSP]TNDNPFDYTWDRDSGLV 84
 Db 168 STISSWIKKQEGISRFAMLRNINP---PGSATGPFIASLSTAGPDVYAWRDALTS 222
 QY 85 KTLVLDLFR---NGDTSLSTIENYISQAIVOCISNPNSGDLSSGAGLGCBPKENDEATYT 141
 Db 223 NVIVYEYNTLGSNTKTLVNLKOVTFVKTSSTVCN----CLGEPKENDASGFT 276

QY 142 GS[G]RPPQDGPA[RATAMIGFG-QMLDNGT]STATIDIVPLVYRNDLSSYQAQWNQTYD 200
 277 GAM[G]RPQDGPA[RATATLFDASYLQ]TKDASVYTGTLKPAIFKDLIYVUNWSNGCFD 336

Db 337 LWEEVNGG[SFTT]AVQH[ALVEGSAFA]TAVGSS--CSVCDSOAPEILCYLOSTWTGSTIL 258

QY 201 LWEEVNGG[SFTT]AVQH[ALVEGSAFA]TAVGSS--CSVCDSOAPEILCYLOSTWTGSTIL 258

QY 309 FRSIYTLDGLSSEAVAVGRYPTY---YNGNPFLCTLAACOLYDALQWQKG 363

RP HOMOLOGY AND PREDICTED SECONDARY STRUCTURE.
 RA Tanaka Y., Asikari T., Nakamura N., Kiuchi N., Shibano Y.,
 RA Amachi T., Yoshiumi H.,
 RT "Comparison of amino acid sequences of three glucoamylases and their
 structure-function relationships";
 RL Agric. Biol. Chem. 50:965-969(1986).
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-
 glucose residues successively from non-reducing ends of the chains
 with release of beta-D-glucose.
 CC -1- MISCELLANEOUS: Rhizopus glucoamylase exists in multiple forms,
 CC Gluc 1', Gluc 2, and Gluc 3, all of which hydrolyze gelatinized
 CC starch at similar rates, but only the largest one (Gluc 1) is able
 CC to adsorb raw starch.
 CC -!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D00449; BA00033_1; -.
 DR PIR; JP0001; JP0001.
 DR PIR4064; IGA1.
 DR InterPro; IPR005336; CBM_21.
 DR InterPro; IPR000165; Glyco_trans_15.
 DR InterPro; IPR008228; Glyco_trans_6hp.
 DR Pfam; PF03370; CBM_21_1.
 DR Pfam; PR00723; Glyco_hydro_15_1.
 DR PRINTS; PR00736; GLYHYDRASE5.
 DR PROSITE; PS00820; GLUCOAMYLASE_1.
 KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein;
 KW Signal. 1 25
 FT SIGNAL 1 25
 FT CHAIN 26 604 GLUCOAMYLASE 1 (GLUC 1).
 FT CHAIN 159 604 GLUCOAMYLASE 2 (GLUC 2).
 FT DOMAIN 26 109 GLUCOAMYLASE 3 (GLUC 3) (OR 110-604).
 FT DOMAIN 116 604 ADSORPTION TO RAW STARCH (OR 26-115).
 FT BINDING 279 279 STARCH DEGRADATION (OR 110-604).
 FT ACT_SITE 336 336 SUBSTRATE (BY SIMILARITY).
 FT ACT_SITE 339 339 CATALYTIC BASE (BY SIMILARITY).
 FT ACT_SITE 340 340 GENERAL ACID CATALYST (BY SIMILARITY).
 FT ACT_SITE 340 340 INTERACT WITH SUBSTRATES (BY SIMILARITY).
 SQ SEQUENCE 604 AA; 65162 MW; 78421F1AA93ADB9 CRC64;

Query Match 26.2%; Score 725; DB 1; Length 604;
 Best Local Similarity 36.8%; Pred. No. 1.6e-40; Indels 42; Gaps 10;
 Matches 165; Conservative 71; Mismatches 170;

QY 25 ATUDSWLNNEATARTAATLNNIGADGAWSGADSGIWA[PSP]TNDNPFDYTWDRDSGLV 84
 Db 168 STISSWIKKQEGISRFAMLRNINP---PGSATGPFIASLSTAGPDVYAWRDALTS 222
 QY 85 KTLVLDLFR---NGDTSLSTIENYISQAIVOCISNPNSGDLSSGAGLGCBPKENDEATYT 141
 Db 223 NVIVYEYNTLGSNTKTLVNLKOVTFVKTSSTVCN----CLGEPKENDASGFT 276

QY 142 GS[G]RPPQDGPA[RATAMIGFG-QMLDNGT]STATIDIVPLVYRNDLSSYQAQWNQTYD 200
 277 GAM[G]RPQDGPA[RATATLFDASYLQ]TKDASVYTGTLKPAIFKDLIYVUNWSNGCFD 336

Db 337 LWEEVNGG[SFTT]AVQH[ALVEGSAFA]TAVGSS--CSVCDSOAPEILCYLOSTWTGSTIL 258

QY 201 LWEEVNGG[SFTT]AVQH[ALVEGSAFA]TAVGSS--CSVCDSOAPEILCYLOSTWTGSTIL 258

QY 309 FRSIYTLDGLSSEAVAVGRYPTY---YNGNPFLCTLAACOLYDALQWQKG 363

Db 448 FASLYPINKNLUYSYLVGNISGRYPEDTYNGNNSQGNSWFLAVTGVALYYRAKEWIGNG 507
Qy 364 SLEVTQVSLDFKALYSDAAG-TYSSSSYVSSIVDAVKTFADGEVISVTHAASNGM 422
Db 508 GYVSSISLPPFKFESSATGCKYVGTSPFNNLAQNTIAADRFLSTVOLHARHNGSL 567
Qy 423 SEQYDQSDFGEOISARDITWSYAAALLTAN 450
Db 568 AEEFDRTTGUSGARDITWSHSLITAS 595

RESULT 9

AMYH_SACFI STANDARD; PRT; 519 AA.

ID AMYH_SACFI STANDARD; PRT; 519 AA.

AC P26389; P28745;

DT 01-AUG-1992 (Rel. 23, Created)
15-JUL-1998 (Rel. 35, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DB Glucoamylase GLU1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucosidase) (1,4-alpha-D-glucan glucohydrolase). GLA1.

OS Saccharomyces fululigera ("yeast").

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycopsidae; Saccharomyces; OX NCBI_TaxID=4944;
RN [1]

RC STRAIN=KZ;

RX MEDLINE=931137640; PubMed=1840332;

RA Hostinova E., Balanova J., Gasperik J.; "The nucleotide sequence of the glucoamylase gene GLU1 from Saccharomyces fululigera KZ."; FEMS Microbiol. Lett. 67:103-108(1991).

RN [2]

RP REVISIONS.

RC STRAIN=KZ;

RA Hostinova E.,
RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.

CC -!- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES. ONLY DIFFERS IN 11 POSITIONS WITH GLUCOAMYLASE GLU1.

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CC EMBL: X58117; CAA41120.1; -.

DR InterPro; IPR00165; Glyco_hydro_15.

DR InterPro; IPR008928; Glyco_trans_6hp.

DR Pfam; PF00723; Glyco_hydro_15_1.

DR PIRINS; PR00735; Glycylase15.

DR PROSITE; PS00820; GLUCOAMYLASE_1.

KW Hydrolase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal.

FT SIGNAL 1 27 GLUCOAMYLASE GLA1.

FT CHAIN 28 519 SUBSTRATE (BY SIMILARITY).

FT BINDING 166 166 CATALYTIC BASE (BY SIMILARITY).

FT ACT_SITE 234 234 GENERAL ACID CATALYST (BY SIMILARITY).

FT ACT_SITE 237 237 INTERACT WITH SUBSTRATES (BY SIMILARITY).

FT ACT_SITE 238 238 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 205 205 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ 519 AA; 57542 MW; A15A009A/640053C CRC64;

Best Local Similarity 35.2%; **Pred.** No. 4.3e-37; **Matches** 173; **Conservative** 73; **Mismatches** 169; **Indels** 77; **Gaps** 16; **Matches** 173; **Conservative** 73; **Mismatches** 169; **Indels** 77; **Gaps** 16;

Db 42 RDLDSWLNEATVARTAILNNIGADGAWNNSGADSGIVVASPSTNDPYFTWTRDGL- 82
Qy 24 RATLDWLNEATVARTAILNNIGADGAWNNSGADSGIVVASPSTNDPYFTWTRDGL- 82

Db 42 RDLDSWLNEATVARTAILNNIGADGAWNNSGADSGIVVASPSTNDPYFTWTRDGL- 82

Qy 83 ---VLKLVLDFRNGTSLSLTIENISADAVOGNSINPSG---DISSGAGIGEPKENVDE 137

Db 102 FLTVLVSLEED--NNFNTLAKAVEYYINTSYNLQRTSINPSGSFDDENHKGLGEPKENTDG 159

Qy 138 TAYTGKWWGRPBDGPRLATM----IGFCOMW---DNGYTSSTDIVPLVR 184

Db 160 SAYTGAWGRPGDGPRLAVASYRVLNDVNSINKGKVLUTSGDNFSST-EDIYKNIK 218

Qy 185 NDLSYYAQYWMNTQGYMLWEEVNGSSFTTAVQRALV-----EGSAPATAVSSCS 235

Db 219 PDLEVIGWGSTGFLMEENGRHTTSVQQLAKAYADIASKSDGDANTTSAS 278

Qy 236 WCDSDAREBILCYLQSFWTGS-----FILANPD---SSRSCKDANTLIGSHTFD 281

Db 279 -----TLESYISGSDGGFVNVDVNHVENDLQONSRRGIDSATVYQPLTHD 327

Qy 282 PRACADSDTRPCSPALANKHEUDVSRVYTLGSLSEAVAVGRYBETY---Y 336

Db 328 -IGESESTPFDVNDVTLQSYLBDNKDORYSVNSA-Y-SAGAAGIGRPEDVYQDGS 384

Qy 337 NGNPWFLCTLAAEQLDQYDQKOGGLENT--DVSLDFKALVSDAAT----- 384

Db 385 EGMPWLTAYAQVQVLYWD-ANSSANDTINKNIDFNKYYVUDSTINSQSSD 443

Qy 385 GYSSSSYVSSIVDAVKTFADGFVSVIYTHAASNGMSMSQYDKSDGEOSARDITWSYA 444

Db 444 VTIKSGSDEFNTVADNLVFGDSFLQVLDHINDGSLNEBOLNRVIGYTSAYSILTWSG 503

Qy 445 ALTTANRNRNSV 456

Db 504 ALLEAIRLRNRY 515

RESULT 10

AMYG_SACFI STANDARD; PRT; 519 AA.

ID AMYG_SACFI STANDARD; PRT; 519 AA.

AC P08017;

DT 01-AUG-1998 (Rel. 08, Created)
01-AUG-1998 (Rel. 08, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Glucoamylase GLU1 precursor (EC 3.2.1.3) (Glucan 1,4-alpha-D-glucosidase) (1,4-alpha-D-glucan glucohydrolase). GLU1.

OS Saccharomyces fululigera ("yeast").

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycopsidae; Saccharomyces.

OC OX NCBI_TaxID=4944;
RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=8730799; PubMed=3114236;

RA Itoh T., Ohtsuki I., Yamashita T., Fukui S.; "Nucleotide sequence of the glucoamylase gene GLU1 in the yeast Saccharomyces fululigera"; J. Bacteriol. 169:4171-4176 (1987).

RA [2]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).

RA MEDLINE=98437615; PubMed=975101;

RA Sevcik J., Solovicova A., Hostinova E., Gasperik J., Wilson K.S., Dauter Z.; "Structure of glucoamylase from Saccharomyces fululigera at 1.7-A resolution"; Acta Crystallogr. D 54:854-866 (1998);

CC -!- CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.

CC -!- SIMILARITY: BELONGS TO FAMILY 15 OF GLYCOSYL HYDROLASES. ONLY

CC DIFFERS IN 11 POSITIONS WITH GLUCOAMYLASE GLA1.

CC
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DR EMBL; L25641; AAA83997.1; --.
 DR PDB; 1AXX; 13-MAY-98.
 DR InterPro; IPR000155; Glyco_hydro_15.
 DR Pfam; PF00723; Glyco_hydro_15; 1.
 DR PRINTS; PR0736; GLYDROLASE_15.
 DR PROSITE; PS00820; GLUCOMYLASE_1.
 KW Hydrolase; Glycosidase; Polybaccaride degradation; Glycoprotein;
 KW Signal; 3D-structure.
 FT SIGNAL 1 27
 FT CHAIN 28 519
 FT BINDING 166 519
 FT ACT SITE 234 519
 FT ACT_SITE 237 519
 FT CARBOHYD 115 519
 FT CARBOHYD 127 519
 FT CARBOHYD 205 519
 FT TURN 30 519
 FT TURN 36 519
 FT TURN 42 519
 FT HELIX 45 519
 FT TURN 62 519
 FT STRAND 64 519
 FT TURN 67 519
 FT STRAND 71 519
 FT TURN 76 519
 FT STRAND 79 519
 FT STRAND 85 519
 FT STRAND 89 519
 FT STRAND 93 519
 FT HELIX 95 519
 FT TURN 112 519
 FT HELIX 116 519
 FT TURN 134 519
 FT STRAND 137 519
 FT TURN 138 519
 FT STRAND 140 519
 FT TURN 142 519
 FT HELIX 145 519
 FT STRAND 154 519
 FT TURN 157 519
 FT STRAND 161 519
 FT TURN 171 519
 FT HELIX 173 519
 FT TURN 193 519
 FT TURN 199 519
 FT TURN 202 519
 FT HELIX 209 519
 FT TURN 216 519
 FT HELIX 217 519
 FT TURN 228 519
 FT STRAND 232 519
 FT TURN 233 519
 FT STRAND 235 519
 FT TURN 236 519
 FT HELIX 241 519
 FT HELIX 244 519
 FT TURN 264 519
 FT HELIX 267 519
 FT TURN 287 519
 FT STRAND 293 519
 FT TURN 294 519
 FT STRAND 298 519

FT HELIX 303 307
 FT TURN 308 309
 FT TURN 316 316
 FT HELIX 317 325
 FT TURN 328 329
 FT TURN 338 339
 FT HELIX 341 357
 FT HELIX 359 363
 FT TURN 374 375
 FT STRAND 378 378
 FT STRAND 383 383
 FT STRAND 389 389
 FT HELIX 390 410
 FT TURN 411 411
 FT STRAND 414 417
 FT HELIX 418 420
 FT HELIX 421 427
 FT TURN 428 428
 FT HELIX 431 433
 FT TURN 434 434
 FT TURN 436 437
 FT HELIX 438 440
 FT STRAND 443 446
 FT TURN 448 449
 FT HELIX 451 474
 FT TURN 477 478
 FT STRAND 484 485
 FT TURN 487 489
 FT STRAND 492 493
 FT TURN 492 497
 FT HELIX 496 499
 FT SEQUENCE 519 519
 SQ 519 AA; 57539 MW; BE73015AD1B77652 CRC64;

Query Match 24.0%; Score 64.5; DB 1; Length 519;
 Best Local Similarity 34.8%; Pred. No. 1..e-36; Mismatches 171; Gaps 16;
 Matches 171; Conservative 73; MisMatches 171; Indels 77; Gaps 16;

QY 24 RATLDWSLNEATVARTAILNNGAGDAWVGADSGIVAVASPTDNPDYFTWTRDSCL- 82
 42 RTDLETFDQKKEVSVLYLQLNTIAVPGCOPNNVGPVTIASPTSNPDYYQWTRDSLT 101
 Db QY 83 ---VIKTVLUDFLRNGDTISLUSTIENYISQAQVYQGISMPSG--DLSSAGLIGEPKFNDE 137
 102 FLTVLSEAD--INNFNTLAKAVEYVINTSYNQRTSPSGEDENHKGLBPKFNDG 159
 Db QY 138 TAVGGSWRPQDQGPALLAM-----LGFGQML---DNGYVSTATDIWPLVR 184
 160 SATGAWWRPQDQGPALLAMAYASRYLNDVNSINEGKULTDSDGIDINPSS-EDIYKIK 218
 QY 185 NDLSYVAQWMNQGYDNEEWNQSSFFTAVOHRLV-----EGSAFATVGSCS 235
 219 PDLEYVIGVYWDSTGDFDNLBENQRHFFPSLVOOKALAYAVDIKSFPDDGFANTLSSAS 278
 Db QY 236 WCDSQAPEELCYIQSFWTS-----FILANFD----SSRSRKDANTLGSIHTFD 281
 279 -----TLESVLSGDGGFVNTPVNHTVNPDLQNSRQGLSATVYGPLTHD 327
 Db QY 282 PEACADDSTFQPCSPRALANKHEVVDSPRSIYVTLNDGLSDSEAVERGYPEDTY----Y 336
 328 -IGESSSTPPDVNEYVHQSYVLLDEDKDRIVSVNAY-SAGAAIGYIPEDVYGDSS 384
 Db QY 337 NGNPWFLCTLAALABQLYQMDQGSLEEV--DVSDFP-----KALYSDAT 384
 385 EGNPWFLLATAAYAQPVYKLAYD-AKSASNDITINKINYDFENKYIVDPLSTINSAYQSSDS 443
 QY 385 GTSSSSSTYSSISIYDAVIFTADGFVSIYETHAASNGNSNSEQDKSDGEQQLSARDLTYA 444
 444 VTIKGSPBFTVADLNUVFGDSFLQVLDHINDGSLNEQLNRYVTGYSTGAVSLTWSSG 503
 Db QY 445 ALJTAANNRRENSV 456
 504 ALJFAIRARERKVK 515

RESULT 11	
AMYG_ARXAD	STANDARD; PRT; 624 AA.
DE	P42042; 01-NOV-1995 (Rel. 32, Created)
AC	DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC	10-Oct-2003 (Rel. 42, Last annotation update)
FT	(1,4-alpha-D-glucan glucohydrolase).
GN	GAA.
OS	Arxula adeninivorans (Yeast).
OC	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyctetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
OX	NCBI_TaxID:37620;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	Manteloffel R., Kunze G.; Subramanian D. (1994) to the EMBL/GenBank/DBJ database.
RA	-1 - CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.
CC	-1 - SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-----
CC	INTERPRO: IPR000165; Glyco_hydro_15.
CC	InterPro: IPR008928; Glyco_trans_6hp.
CC	PFAM: PF00723; Glyco_hydro_15_1.
CC	EMBL: 246901; CA86997_1; -.
CC	HSSP: P04064; IGR1.
CC	InterPro: IPR00336; CBM_21.
DR	DR Pfam: PF00370; CBM_21_1.
DR	DR PROSITE: PRO0736; GLYHDRASB15.
DR	DR PRINSITE: PS00820; GLUCOMANLASE_1.
KW	Hydrolyase; Glycosidase; Polysaccharide degradation; Glycoprotein; Signal.
FT	SIGNAL 1 18 POTENTIAL.
FT	CHAIN 19 624 GLUCOMANLASE.
FT	ACT SITE 340 340 CATALYTIC BASE (BY SIMILARITY).
FT	ACT SITE 343 343 GENERAL ACID CATALYST (BY SIMILARITY).
FT	ACT SITE 344 344 INTERACT WITH SUBSTRATES (BY SIMILARITY).
FT	CARBONYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 168 168 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBONYD 582 582 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE 624 AA; 68980 MW; 74C9CFB43FF71B4 CRC64;
Query	Match 23.2%; Score 641.5; DB 1; Length 624;
Matches	Best Local Similarity 32.8%; Pred. No. 5.3e-55; No. 154; Conservative 90; Mismatches 172; Indels 53; Gaps 13;
Oy	27 LDSLW!-SNEAT--VARTAILNIGAGAWMSGADGAGIWWASPSTNPDYFTWTRDSL 82
Db	160 ITWNLKPSNSDQGIAKSFLNNIN----IPGAAPGVIAQSYSBPDYATWWDASL 214
Oy	83 VLKTLIDLFNRGDTSLISTIENIVISQAIVOCGINSFQDLSGGAGCEGPKNVDEAYTG 142
Db	215 VMDVWVNLVLYSAKSEERKPOLYKILFOYAKAG-AQSONDPATISGEGPEPKVLTNTAFTG 273
RESULT 12	
AMYG YEAST	STANDARD; PRT; 549 AA.
ID	P08019; 01-AUG-1988 (Rel. 08, Created)
AC	DT 01-AUG-1988 (Rel. 31, Last sequence update)
CC	10-Oct-2003 (Rel. 42, Last annotation update)
CC	Glucosylate, intracellular sporulation-specific (EC 3.2.1.3) (Glucan 1,4-alpha-glucosidase).
CC	SGA1 OR SGA OR YL059W.
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomyctetales; Saccharomycetaceae; Saccharomycetes.
OX	NCBI_TaxID:4932;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yamashita T., Nakamura M., Fukui S., RT "Gene fusion is a possible mechanism underlying the evolution of RT STAI."
RA	RT MEDLINE=87194600; PubMed=3106330;
RA	RT J Bacteriol. 169:2142-2149(1987).
RA	RT SEQUENCE FROM N.A.
RA	RT STRAIN=S288C / AB972;
RA	RT MEDLINE=9131326; PubMed=9169870;
RA	RA Churcher C.M., Bowman S., Badcock K., Bankier A., Brown D., Chillingworth T., Connor R., Devlin K., Gentles S., Hamlin N., Harris D.E., Horrell T., Hunt S., Jageis K., Jones M., Lye G., Moulie S., Odell C., Pearson D., Ro-Jandream M.A., Rice P., Rowley N., Skelton J., Smith V., Walsh S., Whitehead S., Barrell B.G., RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome IX." RT Nature 387:84-87(1997)
RA	CC -1 - CATALYTIC ACTIVITY: Hydrolysis of terminal 1,4-linked alpha-D-glucose residues successively from non-reducing ends of the chains with release of beta-D-glucose.
CC	-1 - SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
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DR	EMBL; Z38125; CA86882_1; -.
DR	EMBL; M16166; CA83042_1; -.
DR	EMBL; SA1716; CA8871; -.

RESULT 15
 YG10_MENJA STANDARD; PRT; 615 AA.
 AC Q59005; 16-OCT-2001 (Rel. 40, Created)
 DT 18-OCT-2001 (Rel. 40, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Hypothetical glycosyl hydrolase MJ1610 (EC 3.2.1.-).
 GN MJ1610.
 OS Methanococcus jannaschii.
 OC Archaea; Buryarchaeota; Methanococci; Methanococcales;
 OC Methanocoldococcaceae; Methanococcaceae;
 OC NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN_JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE:96331999; PubMed=8888087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock G.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geohagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii";
 RL Science 273:1058-1073(1996)
 CC --!- SIMILARITY: Belongs to family 15 of glycosyl hydrolases.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U67601; AAB99630.1; --.
 DR
 DR TIGR; MJ1610; --.
 DR InterPro; IPR000165; Glyco_hydro_15.
 DR InterPro; IPR008928; Glyco_trans_6hp.
 DR InterPro; IPR006465; Oligosac_anhyd1.
 DR Pfam; PF00723; GLYCO_hydro_15; 1.
 DR TIGRFAMS; TIGR01577; oligosac_anhyd1; 1.
 DR PROSITE; PS00820; GLUCOAMYLASE_1.
 KW Hypothetical protein; Hydrolase; Glycosidase; Complete proteome.
 FT SITE ACT_SITE 406 406 GENERAL_ACID_CATALYST (BY SIMILARITY)
 FT ACT_SITE 407 407 INTERACT_WITH_SUBSTRATES (BY SIMILARITY).
 FT SEQUENCE 615 AA; 72007 MN; 2B37EBB9FP0357BE5 CRC64;

Query Match
 Best Local Similarity 8.0%; Score 221.5; DB 1; Length 615;
 Matches 101; Conservative 46; Pred. No. 2.9e-07; Indels 165; Gaps 20;

QY 59 GIIVVAPSTDNDPYFTWTRDSDGLVLTKLVLDFRNQDSIISLTTEINYSAQATVOQISNP 118
 Db 284 GGIIRAPSL-HPDTRIVWGRD-GSYIYSTAIDL-----GIRNIPDRFFFMSKIQ----- 331
 QY 119 SGDLSGAGIGEPEKFENVDTAVICSW-----GRPQRQGPALARATM---TGFGQML 167
 Db 332 -----NAD----GSWLQNYVYNGKP-----RLTAIQTQIGSILWAM 364
 QY 168 DNGTISTATDVWVLVRNDLSIYVQIWNQTG-----YDLWEWINGSSFF 211
 Db 365 DVHVRLL-----GDKKFWERYWNTIEKAANYRLVLAUNTPCFLWEERFGVFAV 414
 QY 212 TIAVORHALVEGSAFATAV-----GSSCSMCDSQAPEELCYLQSFWTGSPFLANFD 262
 Db 415 TMGATYAGLJKCKAYSMSKANRKDKVKGKTIETLKHEWPKRFXLE-----D 461

QY 253 SSRSGKDNTLUGSIHTPDEAACDSTFQESPRAHLKENVUDSPRSIYVTLNGIDS 322
 Db 462 EERFAKSINPL-----DKTIDTSILGLSYVPFNLD---VDDEMIKT-----A 501
 QY 323 EAV-----AVGRVEDTYINGNWFLCLILAA---EQYDALYQMDKGQSLEVTV 370
 Db 502 EAIEKAFKYKVSGIGRPFEDIVFGGNPMWITLWLSLYRRLYKVKEDDNGA---DI 557
 QY 371 SJDPFKALYSDAATGTSSSSSTYSSIVDAVKTfadgfvsvivethaangsmsqydksd 430
 Db 558 YLOKSKKLFNWVWVYKF-----DGLPPEQIHKEL 586
 QY 431 GBQLSARDULTWYAAALL 447
 Db 587 GVPMSAMPILGWSNAMFL 603